OM protein - protein search, using sw model

Run on: April 3, 2006, 08:18:31 ; Search time 188 Seconds
(without alignments)
366.928 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 780
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	775	99.4	157	2	AAR62465	Aar62465 Tumour ne
2	774	99.2	157	1	AAP60524	Aap60524 Sequence
3	774	99.2	157	1	AAP70095	Aap70095 Tumour ne
4	774	99.2	157	1	AAP70144	Aap70144 Amino aci
5	774	99.2	157	2	AAR14270	Aar14270 Human TNF
6	774	99.2	157	2	AAR14112	Aar14112 Neutrophi
7	774	99.2	157	2	AAR27747	Aar27747 Human tum
8	774	99.2	157	2	AAR42679	Aar42679 Human Tum
9	774	99.2	157	2	AAR38069	Aar38069 Human TNF
10	774	99.2	157	2	AAR62463	Aar62463 Tumour ne
11	774	99.2	157	2	AAR60243	Aar60243 Human TNF
12	774	99.2	157	2	AAR57437	Aar57437 Human tum
13	774	99.2	157	2	AAW28530	Aaw28530 Human TNF
14	774	99.2	157	2	AAW40819	Aaw40819 Human tum
15	774	99.2	157	2	ABB08912	Abb08912 Human tum
16	774	99.2	157	2	AAY23242	Aay23242 Human tum
17	774	99.2	157	4	AAG79124	Aag79124 Amino aci
18	774	99.2	157	4	AAE10848	Aae10848 Human tum
19	774	99.2	157	4	AAG67761	Aag67761 Amino aci
20	774	99.2	157	4	AAB74783	Aab74783 Wild type
21	774	99.2	157	5	AAE18373	Aae18373 Human mat
22	774	99.2	157	5	AAM51166	Aam51166 Tumour ne
23	774	99.2	157	5	ABB76561	Abb76561 Human tum
24	774	99.2	157	5	ABG70571	Abg70571 Human tum
25	774	99.2	157	5	ABP54869	Abp54869 Human tum
26	774	99.2	157	5	AAB47940	Aab47940 Human tum
27	774	99.2	157	5	ABP54787	Abp54787 Human tum
28	774	99.2	157	5	ABG76348	Abg76348 Human ful
29	774	99.2	157	6	ABU09888	Abu09888 Human tum
30	774	99.2	157	6	ABG72947	Abg72947 Human tum
31	774	99.2	157	6	ABG75765	Abg75765 Human TNF
32	774	99.2	157	6	ABG75772	Abg75772 Human TNF
33	774	99.2	157	6	ABU63586	Abu63586 Human tum
34	774	99.2	157	7	ADC46568	Adc46568 Human tum
35	774	99.2	157	7	ADC61354	Adc61354 Human TNF
36	774	99.2	157	7	ADC81608	Adc81608 Human tum
37	774	99.2	157	7	ADD44654	Add44654 Human tum
38	774	99.2	157	7	ADD89878	Add89878 Human tum
39	774	99.2	157	7	ADE06773	Ade06773 Human ant
40	774	99.2	157	7	ABW02400	Abw02400 Human tum
41	774	99.2	157	7	ADE96348	Ade96348 Human tum
42	774	99.2	157	7	ABW02035	Abw02035 Human tum
43	774	99.2	157	7	ADF91146	Adf91146 Human tum
44	774	99.2	157	7	ADG27428	Adg27428 Human tum
45	774	99.2	157	7	ABW02652	Abw02652 Human mat
46	774	99.2	157	7	ADJ63985	Adj63985 Recombina
47	774	99.2	157	7	ADM15642	Adm15642 Human tum
48	774	99.2	157	7	ADM83147	Adm83147 Human tum
49	774	99.2	157	8	ADF89614	Adf89614 Human tum
50	774	99.2	157	8	ADH10159	Adh10159 Human tum
51	774	99.2	157	8	ADH10158	Adh10158 Human tum
52	774	99.2	157	8	ADI29703	Adi29703 Human TNF
53	774	99.2	157	8	ADO24650	Ado24650 Human TNF
54	774	99.2	157	8	ADP22359	Adp22359 Human tum
55	774	99.2	157	8	ADR01199	Adr01199 Human tum
56	774	99.2	157	8	ADQ60272	Adq60272 Human tum
57	774	99.2	157	8	ADP47316	Adp47316 Human tum
58	774	99.2	157	8	ADS64654	Ads64654 Human tum
59	774	99.2	157	9	ADX97595	Adx97595 Human tum
60	774	99.2	157	9	ADZ19071	Adz19071 Human tum
61	774	99.2	157	9	ADZ72362	Adz72362 Human tum
62	774	99.2	157	9	AEB45417	Aeb45417 Human TNF
63	774	99.2	158	1	AAP60525	Aap60525 Sequence
64	774	99.2	158	1	AAP60533	Aap60533 Sequence
65	774	99.2	158	1	AAP60532	Aap60532 Plasmid 1
66	774	99.2	158	1	AAP70635	Aap70635 Sequence
67	774	99.2	158	1	AAP81069	Aap81069 Sequence
68	774	99.2	158	1	AAP94762	Aap94762 Polypepti
69	774	99.2	158	1	AAP95650	Aap95650 Antitumou
70	774	99.2	158	1	AAP91026	Aap91026 Human tum
71	774	99.2	158	1	AAP93188	Aap93188 Synthetic
72	774	99.2	158	2	AAR05807	Aar05807 Polypepti
73	774	99.2	158	2	AAR05613	Aar05613 Antitumou
74	774	99.2	158	2	AAR07901	Aar07901 Human TNF
75	774	99.2	158	2	AAR04115	Aar04115 Modified
76	774	99.2	158	2	AAR20625	Aar20625 Synthetic
77	774	99.2	158	2	AAR88592	Aar88592 Human met
78	774	99.2	158	2	AAR88591	Aar88591 Human met
79	774	99.2	158	4	AAY72933	Aay72933 Human mat
80	774	99.2	158	5	AAM49766	Aam49766 Human TNF
81	774	99.2	158	6	AAO30461	Aao30461 Human wil
82	774	99.2	158	8	ADU51444	Adu51444 Human TNF
83	774	99.2	159	1	AAP71174	Aap71174 Sequence
84	774	99.2	160	1	AAP80161	Aap80161 Biosynthe
85	774	99.2	164	4	AAB82901	Aab82901 Histidine
86	774	99.2	164	6	ABR42163	Abr42163 His-tagge
87	774	99.2	164	9	ADZ56235	Adz56235 Histidine
88	774	99.2	164	9	AEC10124	Aec10124 Human TNF
89	774	99.2	170	6	ADA00722	Ada00722 Human TNF
90	774	99.2	173	6	AAO30470	Aao30470 Human TNF
91	774	99.2	177	7	ABW02655	Abw02655 Human pro
92	774	99.2	180	4	AAY72934	Aay72934 OmpA sign
93	774	99.2	193	2	AAW48246	Aaw48246 Tumour ne
94	774	99.2	193	2	AAW90067	Aaw90067 Human TNF
95	774	99.2	193	5	ABG73877	Abg73877 FLAG tagg
96	774	99.2	193	5	AAM50621	Aam50621 Tumour ne
97	774	99.2	193	7	ADC28285	Adc28285 Peptide t

98	774	99.2	232	7	ABW02665	Abw02665 Human pro
99	774	99.2	233	1	AAP50096	Aap50096 Sequence
100	774	99.2	233	1	AAP60605	Aap60605 Sequence

ALIGNMENTS

RESULT 1
AAR62465
ID AAR62465 standard; protein; 157 AA.
XX
AC AAR62465;
XX
DT 25-MAR-2003 (revised)
DT 05-JUN-1995 (first entry)
XX
DE Tumour necrosis factor-alpha mutein K65A.
XX
KW Human; tumour necrosis factor; TNF; TNF-a; expression; mutein; mutation;
KW receptor; affinity; therapeutic; diagnostic; cancer therapy; cancer;
KW obesity; septic shock; meningitis.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 65
FT /label= Lys to Ala
XX
PN EP619372-A1.
XX
PD 12-OCT-1994.
XX
PF 17-MAR-1994; 94EP-00104154.
XX
PR 29-MAR-1993; 93EP-00810224.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Banner D, Lesslauer W, Loetscher H, Stueber D;
XX
DR WPI; 1994-311810/39.
DR N-PSDB; AAQ87684.
XX
PT New human TNF-a muteins with higher affinity for p75-TNFR - useful e.g.
PT for cancer therapy, treatment of obesity and toxic shock.
XX
PS Claim 4; Page 15; 53pp; English.
XX
CC The amino acid sequence of the mutated human tumour necrosis factor alpha
CC (TNF-a). The mutein differs from the wild type at position 65 with a
CC change from a Lys residue to a Ala residue. The gene encoding the protein
CC is placed in the expression plasmid pDS56/RBSII and called
CC pDS56/RBSII,SphI-TNFa(K65A). The expression of the wild type or mutein
CC proteins is regulated by the lac repressor present on the plasmid pREP4.
CC The gene encoding the protein is mutated at specific sites resulting in a
CC series of mutated proteins (AAR62464-83 and AAR63093-103). The biological
CC activities of TNF are mediated via specific receptors of mol. wt. 55 and
CC 75 kDa called p55-TNF-R and p75-TNF-R respectively. The mutated proteins
CC presented have a higher affinity for the human p75-TNF receptor than for
CC the p55-TNF receptor. The mutated proteins can be used in a variety of
CC therapeutic or diagnostic applications including cancer therapy,
CC treatment of obesity, septic shock or bacterial meningitis. (Updated on
CC 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 157 aa;

Query Match 99.4%; Score 775; DB 2; Length 157;
Best Local Similarity 96.2%; Pred. No. 1.2e-74;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFAGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
```

RESULT 2
AAP60524
ID AAP60524 standard; protein; 157 AA.
XX
AC AAP60524;
XX
DT 25-MAR-2003 (revised)
DT 07-AUG-1991 (first entry)
XX
DE Sequence of tumour necrosis factor (TNF).
XX
KW Anticancer agent; antitumour; antimalarial; tumour necrosis factor.
XX
OS Oryctolagus cuniculus.
XX
PN WO8603751-A.
XX
PD 03-JUL-1986.
XX
PF 19-DEC-1985; 85WO-EP000721.
XX
PR 21-DEC-1984; 84US-00684595.
PR 09-OCT-1985; 85US-00785847.
PR 09-OCT-1986; 86WO-US002133.
XX
PA (BIOJ) BIOGEN NV.
PA (FIER/) FIERS W C.
PA (ALLE/) ALLET B.
PA (BIOJ) BIOGEN INC.
XX
PI Fiers WC, Fransen LM, Tavernier JHL, Marmenout ALM, Vanderheyd J;
PI Allet B;
XX
DR WPI; 1986-182891/28.
DR N-PSDB; AAN60442.
XX
PT Mammalian tumour necrosis factors - produced by culturing pro-karyotic
PT hosts transformed with recombinant DNA.
XX
PS Claim 11; Page 66; 93pp; English.
XX
CC TNF-like polypeptides and compsns. are produced by the fermentation of
CC host cells transformed with at least one DNA sequence which codes for a
CC mammalian TNF-like polypeptide operatively linked to an expression
CC control sequence in the transformed host. (Updated on 25-MAR-2003 to
CC correct PA field.)
XX
SQ Sequence 157 AA;

Query Match 99.2%; Score 774; DB 1; Length 157;
Best Local Similarity 96.2%; Pred. No. 1.5e-74;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

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              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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                ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
```

RESULT 3
AAP70095
ID AAP70095 standard; protein; 157 AA.
XX
AC AAP70095;
XX
DT 04-APR-1991 (first entry)
XX
DE Tumour necrosis factor.
XX
KW Plasmid; tumour necrosis factor; antitumour agent.
XX
OS Escherichia coli.
XX
PN EP220482-A.
XX
PD 06-MAY-1987.
XX
PF 19-SEP-1986; 86EP-00112941.
XX
PR 30-SEP-1985; 85JP-00217740.
XX
PA (SUNR) SUNTORY LTD.
XX
PI Oshima T, Tanaka S, Matsukura S;
XX
DR WPI; 1987-124161/18.
XX
PT New plasmid for efficient tumour necrosis factor prodn. - comprises
PT plasmid with DNA fragment having phage-gene derived promoter region and E
PT coli derived transcription termination sequence.
XX
PS Claim 6; Page 17-18; 31pp; English.
XX
CC Tumour necrosis factor can be expressed using a plasmid comprising a
CC phage gene-derived promoter region upstream of the TNF structural gene
CC and an E.coli trp a gene terminator joined immediately downstream of a
CC base sequence encoding the termination of translation of the structural
CC gene. The plasmid is capable of efficient expression of TNF on a large
CC scale and with high purity. The transformants may achieve a TNF activity
CC 40-300 times as great as with prior transformants. TNF may comprise at
CC least 40% of total cell protein. The plasmid lacks a pBR322 derived
CC repressor of primer gene. TNF is an antitumour agent
XX
SQ Sequence 157 AA;

```
  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

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              |||| |||||||||||||||||||||| ||||||| |||||||||||||| ||||||||
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Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 4
AAP70144
ID AAP70144 standard; protein; 157 AA.
XX
AC AAP70144;
XX
DT 03-OCT-2002 (revised)
DT 13-MAY-1991 (first entry)
XX
DE Amino acid sequence of mature tumour necrosis factor (TNF).
XX
KW Tumour necrosis factor analogue; lymphokine; anti-tumour.
XX
OS Homo sapiens.
XX
PN EP220966-A.
XX
PD 06-MAY-1987.
XX
PF 30-OCT-1986; 86EP-00308484.
XX
PR 30-OCT-1985; 85US-00792815.
PR 22-MAY-1986; 86US-00866213.
XX
PA (CETU) CETUS CORP.
XX
PI Lin LSL, Dorin G, Yamamoto R, Hanisch WH, Thomson JW, Wolfe SN;
XX
DR WPI; 1987-124486/18.
XX
PT Purified recombinant tumour necrosis factor compsn. - obtd. by using a
PT hydrophobic matrix to retain the factor followed by chromatographic
PT elution.
XX
PS Disclosure; Fig 3; 25pp; English.
XX
CC Specific examples of TNF analogues include N-terminally deleted species
CC of the protein, including those having deletions of the N-terminal
CC 1,2,3,4,5,6,7,8,9,10,14, and 31 AA's of the SQ in AAP70144. Muteins
CC lacking up to and including the first ten AA's at the N-terminus have
CC been found to have comparable or greater specific activities as compared
CC to the TNF of the SQ shown in AAP70144. Other muteins of TNF covered by
CC the method of the invention include species of TNF in which any or all of
CC the cysteine residues have been converted to serine or other neutral AA's
CC for example, glycine or alanine. In general, neutral AA replacements of
CC the cysteine at position 69 result in active TNF proteins. It appears
CC that the cysteine at position 101 is also dispensable. (Updated on 03-OCT
CC -2002 to add missing OS field.)
XX
SQ Sequence 157 AA;

```
  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 5
AAR14270
ID AAR14270 standard; peptide; 157 AA.
XX
AC AAR14270;
XX
DT 09-JAN-1992 (first entry)
XX
DE Human TNF.
XX
KW Tumour necrosis factor; cytotoxic; metastasis.

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XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .18
FT                   /label= #301
FT   Peptide         13. .26
FT                   /label= #306
FT   Peptide         22. .40
FT                   /label= #307
FT   Peptide         43. .58
FT                   /label= #302
FT                   /note= " claim 2 "
FT   Peptide         54. .68
FT                   /label= #308
FT                   /note= " claim 3"
FT   Peptide         63. .83
FT                   /label= #304
FT   Peptide         70. .80
FT                   /note= " claim 7 "
FT   Peptide         73. .94
FT                   /label= #309
FT                   /note= " claim 5 "
FT   Peptide         79. .89
FT                   /label= #323
FT   Peptide         81. .94
FT                   /note= " claim 6 "
FT   Peptide         94. .109
FT                   /label= #303
FT   Peptide         111. .120
FT                   /label= #275
FT   Peptide         132. .150
FT                   /label= #305
FT                   /note= " claim 4 "
XX
PN   WO9114702-A.
XX
PD   03-OCT-1991.
XX
PF   19-MAR-1990;   90AU-00009156.
XX
PR   19-MAR-1990;   90AU-00009156.
PR   22-NOV-1990;   90AU-00003477.
XX
PA   (PEPT-) PEPTIDE TECHN LTD.
XX
PI   Rathjen D,  Aston R;
XX
DR   WPI; 1991-310534/42.
XX
PT   New cytotoxic and/or proliferation-inhibiting polypeptide fragments -
PT   useful in treatment of tumours with reduced side effects.
XX
PS   Claim 1; Fig 1; 35pp; English.
XX
CC   The peptide fragments indicated in the feature table have cytotoxic
CC   and/or inhibition of proliferation effects on tumour cells. The peptides
CC   may be co-administered with whole TNF alpha or with a cyto-toxic drug
XX
SQ   Sequence 157 AA;

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 6
AAR14112
ID   AAR14112 standard; peptide; 157 AA.
XX
AC   AAR14112;
XX
DT   11-DEC-1991  (first entry)
XX
DE   Neutrophil stimulating peptide.
XX
KW   hTNF; AIDS; cancer; inflammatory syndromes; rheumatoid arthritis;
KW   adult respiratory distress syndrome; human tumour necrosis factor.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Peptide         1. .18
FT                   /label= peptide 301
FT   Peptide         13. .26
FT                   /label= peptide 306
FT   Peptide         22. .40
FT                   /label= peptide 307
FT   Peptide         43. .58
FT                   /label= peptide 302
FT   Peptide         54. .68
FT                   /label= peptide 308
FT                   /note= "neutrophil stimulating activity and selective
FT                   effects on neutrophil degranulation"
FT   Peptide         63. .83
FT                   /label= peptide 304
FT                   /note= "neutrophil stimulating activity"
FT   Peptide         70. .80
FT                   /label= peptide 395
FT                   /note= "neutrophil stimulating activity"
FT   Peptide         73. .94
FT                   /label= peptide 309
FT                   /note= "neutrophil stimulating activity"
FT   Peptide         76. .84
FT                   /label= peptide 393
FT   Peptide         79. .89
FT                   /label= peptide 323
FT   Peptide         81. .94
FT                   /label= peptide 394
FT   Peptide         84. .94
FT                   /label= peptide 396
FT   Peptide         94. .109
FT                   /label= peptide 303
FT   Peptide         111. .120
FT                   /label= peptide 275
FT   Peptide         132. .150
FT                   /label= peptide 305
XX
PN   WO9113908-A.
XX
PD   19-SEP-1991.
XX
PF   12-MAR-1990;   90AU-00009065.
XX
PR   12-MAR-1990;   90AU-00009065.
XX
PA   (PEPT-) PEPTIDE TECHN LTD.
XX
PI   Rathjen DA,  Ferrante A;
XX
DR   WPI; 1991-295580/40.
XX
PT   New neutrophil stimulating peptide(s) derived from human TNF - useful for
PT   treating depressed neutrophil function in e.g. AIDS and cancer, and
```

```
PT   inflammatory syndrome in e.g. rheumatoid arthritis.
XX
PS   Disclosure; Fig 1; 27pp; English.
XX
CC   The amino acid sequence codes for human tumour necrosis factor. Peptides
CC   derived from this sequence have neutrophil stimulating activity. The
CC   peptides were synthesised using the Fmoc-polyamide method of solid
CC   peptide synthesis. Treatment with the peptides can be used to restore
CC   depressed or aberrant neutrophil activity without causing the side
CC   effects associated with the therapeutic use of the whole TNF molecule.
CC   Such peptides can be used in the treatment of individuals suffering from
CC   AIDS, cancer or inflammatory syndromes e.g. rheumatoid arthritis or adult
CC   respiratory distress syndrome
XX
SQ   Sequence 157 AA;

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 7
AAR27747
ID   AAR27747 standard; protein; 157 AA.
XX
AC   AAR27747;
XX
DT   25-MAR-2003  (revised)
DT   03-MAR-1993  (first entry)
XX
DE   Human tumour necrosis factor alpha.
XX
KW   hTNF; monoclonal antibody; sepsis syndrome, cachexia, microbial;
KW   infection; rheumatoid arthritis; inflammation.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          1. .20
FT                   /note= "putative receptor binding portion"
FT   Region          11. .13
FT                   /note= "putative receptor binding portion"
FT   Region          37. .42
FT                   /note= "putative receptor binding portion"
FT   Region          49. .57
FT                   /note= "putative receptor binding portion"
FT   Region          59. .80
FT                   /note= "epitope for Ab binding"
FT   Region          87. .108
FT                   /note= "epitope for Ab binding"
FT   Region          155. .157
FT                   /note= "putative receptor binding portion"
XX
PN   WO9216553-A1.
XX
PD   01-OCT-1992.
XX
PF   18-MAR-1992;   92WO-US002190.
XX
PR   18-MAR-1991;   91US-00670827.
XX
PA   (UYNY ) UNIV NEW YORK STATE.
PA   (CENZ ) CENTOCOR INC.
XX
PI   Le J,  Vilcek J,  Daddona PE,  Ghrayeb J,  Knight DM,  Siegel SA;
XX
DR   WPI; 1992-349155/42.
XX
PT   Monoclonal and chimeric antibodies to human TNF - useful for treating
PT   sepsis syndrome, cachexia, microbial infections, rheumatoid arthritis,
PT   inflammation, etc.
XX
PS   Claim 22; Page 77; 105pp; English.
XX
CC   Anti-TNF antibodies were prepd. which bound to an epitope of at least 5
CC   amino acids of residues 87-108 or both of residues 59-80 and 87-108 of
CC   human tumour necrosis factor alpha, but do not bind known or putative
CC   receptor binding portions of TNF, such as those shown in the features
CC   table. The antibodies may be prepd. by hybridomas or recombinantly and
CC   may be used for in vivo treatment and diagnosis of human pathologies
CC   associated with TNF e.g. sepsis syndrome, cachexia, circulatory collapse
CC   and shock resulting from acute or chronic bacterial infection, acute and
CC   parasitic or infectious processes, including bacterial, viral and fungal
CC   infections, acute and chronic immune and autoimmune pathologies such as
CC   sarcoidosis and Crohn's disease, vascular inflammatory pathologies such
CC   as disseminated intravascular coagulation, graft vs. host disease,
CC   Kawasaki's disease and malignant tumours. The antibodies may be used in
CC   combination with TNF therapy, e.g. cancer therapy to remove the undesired
CC   side effects. They may also be used to remove TNF from fluids, tissues or
CC   cells, to detect or quantitate TNF and for blocking TNF activity in vivo,
CC   in situ and in vitro. (Updated on 25-MAR-2003 to correct PN field.)
CC   (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ   Sequence 157 AA;

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 8
AAR42679
ID   AAR42679 standard; protein; 157 AA.
XX
AC   AAR42679;
XX
DT   25-MAR-2003  (revised)
DT   19-APR-1994  (first entry)
XX
DE   Human Tumour Necrosis Factor alpha.
XX
KW   Plasmid pDS56/RBSII,SphI-TNF-alpha; mutein; inflammation; obesity;
KW   septic shock; treatment; mutagenic PCR; cytokine.
XX
OS   Homo sapiens.
XX
PN   EP563714-A2.
XX
PD   06-OCT-1993.
XX
PF   20-MAR-1993;   93EP-00104591.
XX
```

PR 02-APR-1992; 92EP-00810249.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Lesslauer W, Loetscher H, Stueber D;
XX
DR WPI; 1993-313109/40.
DR N-PSDB; AAQ49223.
XX
PT New human Tumour Necrosis Factor mutein(s) - have amino acid change at
PT position 86, for selective binding affinity to the P55-TNF-Receptor.
XX
PS Disclosure; Fig 1b; 29pp; English.
XX
CC The human TNF-alpha expression plasmid pDS56/RBSII,SphI-TNF-alpha was
CC used as the source of TNF-alpha gene for preparing the various TNF-alpha
CC muteins of the invention. Mutagenic PCR was used on the wild-type
CC template to introduce amino acid substitutions at sites affecting binding
CC specificity. The muteins retain binding activity to the human p55-TNF-
CC Receptor but do not bind to the human p75-TNF- Receptor. Consequently,
CC the muteins have lower systemic toxicity and only elicit some of the
CC activities of wild-type TNF-a. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
SQ Sequence 157 AA;

Query Match 99.2%; Score 774; DB 2; Length 157;
Best Local Similarity 96.2%; Pred. No. 1.5e-74;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
Db 61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy 121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

RESULT 9
AAR38069
ID AAR38069 standard; protein; 157 AA.
XX
AC AAR38069;
XX
DT 14-OCT-1993 (first entry)
XX
DE Human TNF-alpha.
XX
KW Withdrawal symptom; tumour necrosis factor; narcotic; nicotine; morphine;
KW thymosin; alcohol.
XX
OS Homo sapiens.
XX
PN JP05117161-A.
XX
PD 14-MAY-1993.
XX
PF 23-OCT-1991; 91JP-00337489.
XX
PR 23-OCT-1991; 91JP-00337489.
XX
PA (SOMA/) SOMA G.
PA (MIZU/) MIZUNO D.
XX
DR WPI; 1993-191442/24.
XX
PT Drugs for treating alcohol, morphine narcotics or nicotine withdrawal
PT symptoms - contg. tumour necrosis factor-alpha, thymosin tumour necrosis
PT factor fused cpd. or murine tumour necrosis factor-alpha prepd. from
PT macrophage of human or animal.
XX
PS Disclosure; Page 2-3; 5pp; Japanese.
XX
CC Drugs acting on withdrawal symptoms contain TNF, esp. TNF-alpha (AAR38069
CC and AAR38077), rTNF-S-AM1 (AAR38070), rTNF-S-AM2 (AAR38071), thymosin-
CC beta4-TNF fused cpd. (AAR38072-76). The drugs are effective in treatment
CC of withdrawal symptoms caused by habitual use of alcohol, morphine
CC narcotics or nicotine in humans or animals (e.g. swine, dog, cat,
CC chicken). The drugs may be administered as TNF at a dose of 10ng-10mg
CC orally or 5ng-1mg i.v. or 50ng-50mg percutaneously a day for a human
CC adult. In animals, the drugs may be administered according to the human
CC dosage (1/60 per kg body wt.)
XX
SQ Sequence 157 AA;

Query Match 99.2%; Score 774; DB 2; Length 157;
Best Local Similarity 96.2%; Pred. No. 1.5e-74;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
Db 61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy 121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

RESULT 10
AAR62463
ID AAR62463 standard; protein; 157 AA.
XX
AC AAR62463;
XX
DT 25-MAR-2003 (revised)
DT 02-JUN-1995 (first entry)
XX
DE Tumour necrosis factor-alpha protein.
XX
KW Human; tumour necrosis factor; TNF; TNF-a; expression; mutein; mutation;
KW receptor; affinity; therapeutic; diagnostic; cancer therapy; cancer;
KW obesity; septic shock; meningitis.
XX
OS Homo sapiens.
XX
PN EP619372-A1.
XX
PD 12-OCT-1994.
XX
PF 17-MAR-1994; 94EP-00104154.
XX
PR 29-MAR-1993; 93EP-00810224.
XX
PA (HOFF) HOFFMANN LA ROCHE & CO AG F.
XX
PI Banner D, Lesslauer W, Loetscher H, Stueber D;
XX
DR WPI; 1994-311810/39.
DR N-PSDB; AAQ73431.
XX
PT New human TNF-a muteins with higher affinity for p75-TNFR - useful e.g.
PT for cancer therapy, treatment of obesity and toxic shock.
XX
PS Disclosure; Page 28-31; 53pp; English.
XX
CC The amino acid sequence of the human wild type tumour necrosis factor
CC alpha (TNF-a). The gene encoding the protein is placed in the expression

```
CC   plasmid pDS56/RBSII and called pDS56/RBSII,SphI-TNFa. The expression of
CC   the wild type or mutein proteins is regulated by the lac repressor
CC   present on the plasmid pREP4. The gene encoding the protein is mutated at
CC   specific sites resulting in series of mutated proteins (AAR62464-83 and
CC   AAR63093-103). The biological activities of TNF are mediated via specific
CC   receptors of mol. wt. 55 and 75 kDa called p55-TNF-R and p75-TNF-R
CC   respectively. The mutated protein presented have a higher affinity for
CC   the human p75-TNF receptor than for the p55-TNF receptor. The mutated
CC   proteins can be used in a variety of therapeutic or diagnostic
CC   applications including cancer therapy, treatment of obesity, septic shock
CC   or bacterial meningitis. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 157 AA;

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 11
AAR60243
ID   AAR60243 standard; peptide; 157 AA.
XX
AC   AAR60243;
XX
DT   25-MAR-2003  (revised)
DT   16-MAR-1995  (first entry)
XX
DE   Human TNF-alpha.
XX
KW   TNF-alpha; tumor necrosis factor-alpha; tip peptide; mutein; cancer;
KW   sepsis; inflammation; cytokine; metastasis; lectin; adhesion;
KW   mutagenesis.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1. .8
FT                   /note= "in TNF muteins, residues 1-8 are replaced by a
FT                   peptide within the region spanning aa 5-30 of laminin"
FT   Misc-difference 101
FT                   /note= "in TNF muteins, residue 101 is Ser"
FT   Misc-difference 102
FT                   /note= "in TNF muteins, residue 102 is Arg or deleted"
FT   Misc-difference 103
FT                   /note= "in TNF muteins, residue 103 is Trp"
FT   Misc-difference 105
FT                   /note= "in TNF muteins, residue 105 is Pro or Ile or
FT                   residue 105 is Ile and residue 44 is Cys"
FT   Misc-difference 106
FT                   /note= "in TNF muteins, residue 106 is Ser, or residue
FT                   106 is Ser and residue 131 is Cys"
FT   Misc-difference 108
FT                   /note= "In TNF muteins, residue 108 is Phe"
FT   Misc-difference 110
FT                   /note= "In TNF muteins, residue 110 is Lys"
FT   Misc-difference 111. .112
FT                   /note= "In TNF muteins, residues 111-112 are deleted, or
FT                   residue 111 is deleted or Met, or residue 111 is deleted
FT                   and residue 109 is Gln and residue 120 is His"
FT   Misc-difference 115. .116
FT                   /note= "In TNF muteins, residues 115-116 are Ile-Lys"
FT   Misc-difference 115
FT                   /note= "In TNF muteins, residue 115 is Ile or Cys"
FT   Misc-difference 116
FT                   /note= "In TNF muteins, residue 116 is Lys, His or Val"
XX
PN   WO9418325-A1.
XX
PD   18-AUG-1994.
XX
PF   02-FEB-1994;   94WO-EP000286.
XX
PR   03-FEB-1993;   93EP-00400262.
XX
PA   (INNO-) INNOGENETICS NV SA.
XX
PI   Lucas R,  De Baetselier P,  Fransen L,  Sablon E;
XX
DR   WPI; 1994-279746/34.
XX
PT   New tumour necrosis factor -alpha muteins, antibodies and antisense
PT   peptide(s) - used in the treatment of diseases and conditions associated
PT   with the in vivo activities of TNF-A eg cancer, sepsis, inflammation,
PT   etc.
XX
PS   Disclosure; Page 10; 132pp; English.
XX
CC   TNF-alpha muteins were constructed in the tip region (given in AAR60231)
CC   of human TNF-alpha. The mutations resulted in: modulation of lectin-like
CC   activity; reduced toxic activity; modulation of inflammatory activity;
CC   modulated adhesion molecule inducing capacity; reduced metastasis
CC   promoting activity; and/or increased half-life. Muteins of the mouse TNF
CC   (given in AAR60244) may also be produced. (Updated on 25-MAR-2003 to
CC   correct PN field.)
XX
SQ   Sequence 157 AA;

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 12
AAR57437
ID   AAR57437 standard; protein; 157 AA.
XX
AC   AAR57437;
XX
DT   25-MAR-2003  (revised)
DT   13-MAR-1995  (first entry)
XX
DE   Human tumour necrosis factor (wild-type).
XX
KW   Tumour necrosis factor; TNF; mutein; variant; antitumour; toxicity;
KW   haemorrhagic necrosis; antiviral; parasite; malaria.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 1. .7
FT                   /note= "one or more of the first 7 N-terminal amino acids
```

```
FT                   may be deleted"
FT   Misc-difference 4
FT                   /note= "Ser pref. replaced by Arg"
FT   Misc-difference 5
FT                   /note= "Ser pref. replaced by Arg"
FT   Misc-difference 6
FT                   /note= "Arg pref. replaced by Ala"
FT   Misc-difference 7
FT                   /note= "Thr pref. replaced by His or Lys"
FT   Misc-difference 8
FT                   /note= "Pro pref. replaced by Arg"
FT   Misc-difference 9
FT                   /note= "Ser pref. replaced by Lys"
FT   Misc-difference 10
FT                   /note= "Asp pref. replaced by Arg"
FT   Misc-difference 38
FT                   /note= "Ala pref. replaced by Asp"
FT   Misc-difference 39
FT                   /note= "Asn pref. replaced by Asp, Lys or Val"
FT   Misc-difference 40
FT                   /note= "Gly pref. replaced by Asp, Lys or Val"
FT   Misc-difference 41
FT                   /note= "Val pref. replaced by Ser"
FT   Misc-difference 52
FT                   /note= "Ser pref. replaced by Ile, Glu or Lys"
FT   Misc-difference 53
FT                   /note= "Glu pref. replaced by Lys or Leu"
FT   Misc-difference 54
FT                   /note= "Gly pref. replaced by Asp or Val"
FT   Misc-difference 56
FT                   /note= "Tyr pref. replaced by Phe or Glu"
FT   Misc-difference 85
FT                   /note= "Val pref. replaced by Glu or Arg"
FT   Misc-difference 86
FT                   /note= "Ser pref. replaced by Leu, Lys, Glu or Asp"
FT   Misc-difference 87
FT                   /note= "Tyr pref. replaced by Glu or Arg"
FT   Misc-difference 88
FT                   /note= "Gln pref. replaced by Glu"
FT   Misc-difference 127
FT                   /note= "Glu pref. replaced by Ala, Val or Lys"
FT   Misc-difference 128
FT                   /note= "Lys pref. replaced by Ala, Val or Glu"
FT   Misc-difference 129
FT                   /note= "Gly pref. replaced by Glu, Lys or Val"
FT   Misc-difference 156
FT                   /note= "Ala pref. replaced by Asp"
FT   Misc-difference 157
FT                   /note= "Leu pref. replaced by Phe"
XX
PN   DE4404124-A1.
XX
PD   11-AUG-1994.
XX
PF   09-FEB-1994;   94DE-04404124.
XX
PR   09-FEB-1993;   93KR-00001751.
XX
PA   (HANI-) HANIL SYNTHETIC FIBER CO LTD.
XX
PI   Shin H,  Shin N,  Lee I,  Kang S;
XX
DR   WPI; 1994-250457/31.
DR   N-PSDB; AAQ67089.
XX
PT   New tumour necrosis factor muteins and related DNA - also vectors and
PT   transformed cells, with increased antitumour activity and lower toxicity
PT   than wild type protein.
XX
PS   Claim 1; Page 20; 23pp; German.
XX
CC   TNF muteins are claimed, in which at least one amino acid at positions 4-
CC   10, 38-41, 52-54, 56, 85-88, 127-129, 156 or 157 is exchanged for a
CC   different amino acid. Opt. one or more of the first 7 N-terminal amino
CC   acids is deleted. TNF causes haemorrhagic necrosis of tumours; has anti-
CC   viral activity and inactivates some species of malarial parasites. The
CC   muteins have increased antitumour activity and lower toxicity than wild-
CC   type protein. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ   Sequence 157 AA;

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.5e-74;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 13
AAW28530
ID   AAW28530 standard; protein; 157 AA.
XX
AC   AAW28530;
XX
DT   25-MAR-2003  (revised)
DT   11-JAN-1998  (first entry)
XX
DE   Human TNF.
XX
KW   TNF; tumour necrosis factor; Crohn's disease; cA2 antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Region          11. .13
FT                   /label= epitope
FT   Region          37. .42
FT                   /label= epitope
FT   Region          49. .57
FT                   /label= epitope
FT   Region          59. .80
FT                   /label= epitope
FT   Region          87. .108
FT                   /label= epitope
FT   Region          155. .157
FT                   /label= epitope
XX
PN   US5656272-A.
XX
PD   12-AUG-1997.
XX
PF   04-FEB-1994;   94US-00192102.
XX
PR   18-MAR-1991;   91US-00670827.
PR   18-MAR-1992;   92US-00853606.
PR   11-SEP-1992;   92US-00943852.
PR   26-JAN-1993;   93US-00010406.
PR   02-FEB-1993;   93US-00013413.
XX
PA   (CENZ ) CENTOCOR INC.
PA   (UYNY-) UNIV NEW YORK MEDICAL CENT.
XX
PI   Dadonna P,  Le J,  Ghrayeb J,  Knight D,  Siegel SA,  Vilcek J;
XX
DR   WPI; 1997-414547/38.
XX
```

PT Treatment of Crohn's disease - by administering humanised cA2 antibody
PT specific for tumour necrosis factor.
XX
PS Claim 4 and 6; Fig 13; 87pp; English.
XX
CC An anti-TNF chimeric antibody may be administered for treating TNF-alpha
CC mediated Crohn's disease in a human. The anti-TNF chimeric antibody
CC competitively inhibits binding of TNF to monoclonal antibody cA2. The
CC anti-TNF antibody does not bind to one or more epitopes in amino acids 11
CC -13, 37-42, 49-57 or 155-157 of hTNF, but does bind to one or more
CC epitopes included in amino acids between 87-108 or both 87-108 and 59-80
CC of hTNF. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 157 AA;

Query Match 99.2%; Score 774; DB 2; Length 157;
Best Local Similarity 96.2%; Pred. No. 1.5e-74;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
Db 61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy 121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

RESULT 14
AAW40819
ID AAW40819 standard; peptide; 157 AA.
XX
AC AAW40819;
XX
DT 02-APR-1998 (first entry)
XX
DE Human tumour necrosis factor.
XX
KW Tumour necrosis factor; human; hTNF; rheumatoid arthritis; malignancy;
KW anti-TNF chimeric antibody; inhibitor; therapy; diagnosis; infection;
KW chronic inflammatory disease; autoimmune disease;
KW neurodegenerative disease.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 59. .80
FT /note= "epitope recognised by antibody of the invention"
FT Misc-difference 87. .108
FT /note= "epitope recognised by antibody of the invention"
XX
PN US5698195-A.
XX
PD 16-DEC-1997.
XX
PF 18-OCT-1994; 94US-00324799.
XX
PR 18-MAR-1991; 91US-00670827.
PR 18-MAR-1992; 92US-00853606.
PR 11-SEP-1992; 92US-00943852.
PR 29-JAN-1993; 93US-00010406.
PR 02-FEB-1993; 93US-00013413.
PR 04-FEB-1994; 94US-00192061.
PR 04-FEB-1994; 94US-00192093.
PR 04-FEB-1994; 94US-00192102.
XX
PA (CENZ) CENTOCOR INC.
PA (UYNY-) UNIV NEW YORK MEDICAL CENT.
XX
PI Siegel S, Knight D, Vilcek J, Ghrayeb J, Le J, Daddona P;
XX
DR WPI; 1998-051431/05.
XX
PT Treatment of rheumatoid arthritis - with chimeric antibody directed
PT against tumour necrosis factor.
XX
PS Claim 3; Col 97-100; 93pp; English.
XX
CC This sequence represents the human tumour necrosis factor (hTNF).
CC Epitopes of this sequence are recognised by the antibody used in the
CC method of the invention. The method of the invention is for treating
CC rheumatoid arthritis in a human, and comprises administering to the human
CC an effective TNF-inhibiting amount of an anti-TNF chimeric antibody (Ab),
CC where the anti-TNF chimeric Ab comprises a non-human variable region or a
CC TNF antigen binding portion of the variable region, and a human constant
CC region. The method can be used for in vitro, in situ and/or in vivo
CC diagnosis and/or treatment of animal cells, tissues or pathologies
CC associated with the presence of TNF. The Abs used in the method can also
CC be used for removing TNF from a solution or cells, inhibiting one or more
CC biological activities of TNF in vitro, in situ or in vitro. Such removal
CC can include treatment methods of the invention for alleviating symptoms
CC or pathologies involving TNF, such as bacterial, viral or parasitic
CC infections, chronic inflammatory diseases, autoimmune diseases,
CC malignancies and/or neurodegenerative diseases
XX
SQ Sequence 157 AA;

Query Match 99.2%; Score 774; DB 2; Length 157;
Best Local Similarity 96.2%; Pred. No. 1.5e-74;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
Db 1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy 61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
Db 61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy 121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
Db 121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157

RESULT 15
ABB08912
ID ABB08912 standard; protein; 157 AA.
XX
AC ABB08912;
XX
DT 16-JUL-2002 (first entry)
XX
DE Human tumour necrosis factor (TNF) beta-sheet forming portion.
XX
KW Human; TNF; tumour necrosis factor; beta-sheet; fusion protein;
KW recombinant production; Escherichia coli; TNF fusion vector; pT7-T150;
KW pT7-T57.
XX
OS Homo sapiens.
XX
PN KR133475-B1.
XX
PD 21-APR-1998.
XX
PF 04-APR-1994; 94KR-00007018.
XX
PR 04-APR-1994; 94KR-00007018.
XX
PA (HANI-) HANIL SYNTHETIC FIBER CO LTD.
XX
PI Shin H, Jang S, Kim D, Kang S;
XX

DR WPI; 1999-617508/53.
XX
PT USE OF BETA-SHEET FORMING AMINO ACID LEADER SEQUENCE FOR THE PRODUCTION
PT OF PROTEINS.
XX
PS Claim 1; Page 9; 14pp; Korean.
XX
CC The invention relates to a method for the recombinant production of
CC proteins, involving the fusion of a leader sequence capable of forming a
CC beta-sheet to a desired protein. In particular, a protein of interest is
CC expressed in Escherichia coli as a fusion with a beta-sheet forming
CC portion of human tumour necrosis factor (TNF; see ABB08912), and the TNF
CC fusion vectors pT7-T150 and pT7-T57 are used to accomplish this. The
CC present sequence represents a portion of human TNF specifically claimed
CC for use in the method of the invention
XX
SQ Sequence 157 AA;

Query Match 99.2%; Score 774; DB 2; Length 157;
Best Local Similarity 96.2%; Pred. No. 1.5e-74;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Search completed: April 3, 2006, 08:22:09
Job time : 193 secs

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:21:30 ; Search time 22 Seconds
(without alignments)
590.004 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 780
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	774	99.2	157	1	US-07-794-400-1	Sequence 1, Appli
2	774	99.2	157	1	US-08-041-648-2	Sequence 2, Appli
3	774	99.2	157	1	US-08-107-235-1	Sequence 1, Appli
4	774	99.2	157	1	US-08-217-529-2	Sequence 2, Appli
5	774	99.2	157	1	US-08-318-193-86	Sequence 86, Appl
6	774	99.2	157	1	US-08-397-470-1	Sequence 1, Appli
7	774	99.2	157	1	US-08-192-102-1	Sequence 1, Appli
8	774	99.2	157	1	US-08-324-799-1	Sequence 1, Appli
9	774	99.2	157	1	US-08-538-875-1	Sequence 1, Appli
10	774	99.2	157	1	US-08-394-600B-17	Sequence 17, Appl
11	774	99.2	157	1	US-08-500-860A-35	Sequence 35, Appl
12	774	99.2	157	1	US-08-192-861A-1	Sequence 1, Appli
13	774	99.2	157	1	US-08-600-783-5	Sequence 5, Appli
14	774	99.2	157	2	US-08-584-031-13	Sequence 13, Appl
15	774	99.2	157	2	US-08-714-960B-1	Sequence 1, Appli
16	774	99.2	157	2	US-09-133-119-1	Sequence 1, Appli
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19	774	99.2	157	2	US-09-496-118B-7	Sequence 7, Appli
20	774	99.2	157	2	US-08-395-456C-17	Sequence 17, Appl
21	774	99.2	157	2	US-08-487-453A-17	Sequence 17, Appl
22	774	99.2	157	2	US-09-582-450-13	Sequence 13, Appl
23	774	99.2	157	2	US-09-934-465-13	Sequence 13, Appl
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25	774	99.2	157	2	US-09-756-398B-1	Sequence 1, Appli
26	774	99.2	157	4	PCT-US92-02190-1	Sequence 1, Appli
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29	774	99.2	157	6	5180811-1	Patent No. 5180811
30	774	99.2	158	2	US-09-645-415A-4	Sequence 4, Appli
31	774	99.2	177	1	US-08-394-600B-21	Sequence 21, Appl
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36	774	99.2	193	1	US-08-889-909A-3	Sequence 3, Appli
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39	774	99.2	233	1	US-08-323-445A-10	Sequence 10, Appl
40	774	99.2	233	1	US-08-515-903A-10	Sequence 10, Appl
41	774	99.2	233	1	US-08-912-227-3	Sequence 3, Appli
42	774	99.2	233	1	US-08-230-428B-2	Sequence 2, Appli
43	774	99.2	233	2	US-08-883-086-6	Sequence 6, Appli
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45	774	99.2	233	2	US-09-589-287B-3	Sequence 3, Appli
46	774	99.2	233	2	US-09-513-584-3	Sequence 3, Appli
47	774	99.2	233	2	US-09-157-864-9	Sequence 9, Appli
48	774	99.2	233	2	US-10-082-260-5	Sequence 5, Appli
49	774	99.2	233	2	US-09-345-790-3	Sequence 3, Appli
50	774	99.2	233	2	US-09-982-308B-22	Sequence 22, Appl
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60	774	99.2	233	4	PCT-US95-12840-10	Sequence 10, Appl
61	774	99.2	233	6	5422425-2	Patent No. 5422425
62	774	99.2	258	2	US-09-949-016-11027	Sequence 11027, A
63	772	99.0	157	1	US-07-940-605A-5	Sequence 5, Appli
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65	771	98.8	158	6	5182196-2	Patent No. 5182196
66	770	98.7	156	1	US-08-323-445A-19	Sequence 19, Appl
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68	769	98.6	158	1	US-07-794-400-6	Sequence 6, Appli
69	769	98.6	158	1	US-07-794-400-7	Sequence 7, Appli
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71	769	98.6	158	1	US-08-397-470-6	Sequence 6, Appli
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74	768	98.5	158	1	US-07-794-400-4	Sequence 4, Appli
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76	767	98.3	158	1	US-07-794-400-10	Sequence 10, Appl
77	767	98.3	158	1	US-08-397-470-10	Sequence 10, Appl
78	766	98.2	158	1	US-07-794-400-5	Sequence 5, Appli
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82	765	98.1	155	1	US-07-763-512-1	Sequence 1, Appli
83	765	98.1	155	1	US-07-994-469A-1	Sequence 1, Appli
84	765	98.1	158	1	US-07-994-469A-53	Sequence 53, Appl
85	765	98.1	170	6	5180811-11	Patent No. 5180811
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87	765	98.1	187	6	5180811-13	Patent No. 5180811
88	764	97.9	157	1	US-07-668-517-33	Sequence 33, Appl
89	764	97.9	158	1	US-07-668-517-34	Sequence 34, Appl
90	763	97.8	157	1	US-07-994-469A-2	Sequence 2, Appli
91	763	97.8	158	1	US-07-794-400-11	Sequence 11, Appl
92	763	97.8	158	1	US-08-397-470-11	Sequence 11, Appl
93	762	97.7	158	1	US-07-994-469A-98	Sequence 98, Appl
94	761	97.6	158	1	US-07-994-469A-97	Sequence 97, Appl
95	760	97.4	155	1	US-07-994-469A-5	Sequence 5, Appli
96	760	97.4	158	1	US-07-794-400-12	Sequence 12, Appl
97	760	97.4	158	1	US-08-397-470-12	Sequence 12, Appl
98	760	97.4	161	1	US-07-994-469A-61	Sequence 61, Appl
99	760	97.4	163	1	US-07-994-469A-64	Sequence 64, Appl
100	759	97.3	155	1	US-07-994-469A-13	Sequence 13, Appl

ALIGNMENTS

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RESULT 1
US-07-794-400-1
; Sequence 1, Application US/07794400
; Patent No. 5422104
; GENERAL INFORMATION:
;   APPLICANT: Fiers, W.
;   APPLICANT: Tavernier, J.
;   APPLICANT: Van Ostade, X.
;   TITLE OF INVENTION: TNF-Muteins
;   NUMBER OF SEQUENCES: 24
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Hoffmann-La Roche Inc.
;     STREET: 340 Kingsland Street
;     CITY: Nutley
;     STATE: New Jersey
;     COUNTRY: USA
;     ZIP: 07110
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/07/794,400
;     FILING DATE: 19911120
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 90810901.0
;     FILING DATE: 21-NOV-1990
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Krovatin, William
;     REGISTRATION NUMBER: 33256
;     REFERENCE/DOCKET NUMBER: 4105/136-00
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (201) 235-4387
;     TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 157 amino acids
;     TYPE: AMINO ACID
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   ORIGINAL SOURCE:
;     ORGANISM: Homo sapiens
;     TISSUE TYPE: Blood
;     CELL TYPE: Macrophage
US-07-794-400-1

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 2
US-08-041-648-2
; Sequence 2, Application US/08041648
; Patent No. 5486463
; GENERAL INFORMATION:
;   APPLICANT: Lesslauer, Werner
;   APPLICANT: L tscher, Hansruedi
;   APPLICANT: St ber, Dietrich
;   TITLE OF INVENTION: TNF-MUTEINS
;   NUMBER OF SEQUENCES: 17
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: George M. Gould, Esq., Hoffmann-La Roche Inc.
;     STREET: 340 Kingsland Street
;     CITY: Nutley
;     STATE: New Jersey
;     COUNTRY: U.S.A.
;     ZIP: 07110-1199
;   COMPUTER READABLE FORM:
;     MEDIUM TYPE: Floppy disk
;     COMPUTER: IBM PC compatible
;     OPERATING SYSTEM: PC-DOS/MS-DOS
;     SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER: US/08/041,648
;     FILING DATE: 1-APR-1993
;     CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER: EP 92810249.0
;     FILING DATE: 2-APR-1992
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Roseman, Catherine R.
;     REGISTRATION NUMBER: 34240
;     REFERENCE/DOCKET NUMBER: RAN 4105/147
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE: (201) 235-6208
;     TELEFAX: (201) 235-3500
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 157 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-041-648-2

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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RESULT 3
US-08-107-235-1
; Sequence 1, Application US/08107235
; Patent No. 5587457
; GENERAL INFORMATION:
;   APPLICANT: Rathjen, Deborah A
;   APPLICANT: Ferrante, Antonio
;   APPLICANT: Widmer, Fred
;   TITLE OF INVENTION: Neutrophil Stimulating Peptides
;   NUMBER OF SEQUENCES: 19
;   CORRESPONDENCE ADDRESS:
;     ADDRESSEE: Allegretti & Witcoff, Ltd.
;     STREET: 10 S. Wacker Dr.
;     CITY: Chicago
;     STATE: Illinois
```

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;       COUNTRY:  USA
;       ZIP:  60606
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/107,235
;       FILING DATE:  16-AUG-1993
;       CLASSIFICATION:  530
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/930,415
;       FILING DATE:  12-MAR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  McDonnell, John J
;       REGISTRATION NUMBER:  26,949
;       REFERENCE/DOCKET NUMBER:  92,622A
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  312-715-1000
;       TELEFAX:  312-715-1234
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  157 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
;     FEATURE:
;       NAME/KEY:  Peptide
;       LOCATION:  1..157
;       OTHER INFORMATION:  /note= "HUMAN TNF)"
US-08-107-235-1

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 4
US-08-217-529-2
; Sequence 2, Application US/08217529
; Patent No. 5597899
;  GENERAL INFORMATION:
;    APPLICANT:  Banner, David
;    APPLICANT:  Lesslauer, Werner
;    APPLICANT:  Lotscher, Hansreudi
;    APPLICANT:  Stuber, Dietrich
;    TITLE OF INVENTION:  Tumor Necrosis Factor Muteins
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  George M. Gould, Esq., Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  U.S.
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/217,529
;      FILING DATE:  24-MAR-1994
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  EP 93810224.1
;      FILING DATE:  29-MAR-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Roseman, Catherine R
;      REGISTRATION NUMBER:  34240
;      REFERENCE/DOCKET NUMBER:  4105/155
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-6208
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-217-529-2

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              ||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 5
US-08-318-193-86
; Sequence 86, Application US/08318193
; Patent No. 5641663
;  GENERAL INFORMATION:
;    APPLICANT:  GARVIN, Robert T.
;    APPLICANT:  MALEK, Lawrence T.
;    TITLE OF INVENTION:  AN EXPRESSION SYSTEM FOR THE SECRETION
;    TITLE OF INVENTION:  OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
;    TITLE OF INVENTION:  STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
;    TITLE OF INVENTION:  PROTEINS FROM STREPTOMYCES
;    NUMBER OF SEQUENCES:  91
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  1800 Diagonal Road, Suite 500
;      CITY:  Alexandria
;      STATE:  Virginia
;      COUNTRY:  USA
;      ZIP:  22313-0299
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/318,193
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/935,314
;      FILING DATE:
;      APPLICATION NUMBER:  US 07/224,568
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BENT, Stephen A.
```

```
;      REGISTRATION NUMBER:  29,768
;      REFERENCE/DOCKET NUMBER:  18740/116 CACO
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)836-9300
;      TELEFAX:  (703)683-4109
;      TELEX:  899149
;  INFORMATION FOR SEQ ID NO:  86:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-318-193-86

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 6
US-08-397-470-1
; Sequence 1, Application US/08397470
; Patent No. 5652353
;  GENERAL INFORMATION:
;    APPLICANT:  Fiers, W.
;    APPLICANT:  Tavernier, J.
;    APPLICANT:  Van Ostade, X.
;    TITLE OF INVENTION:  TNF-Muteins
;    NUMBER OF SEQUENCES:  24
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hoffmann-La Roche Inc.
;      STREET:  340 Kingsland Street
;      CITY:  Nutley
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07110
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/397,470
;      FILING DATE:  01-MAR-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/794,400
;      FILING DATE:  20-NOV-1991
;      APPLICATION NUMBER:  EP 90810901.0
;      FILING DATE:  21-NOV-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Krovatin, William
;      REGISTRATION NUMBER:  33256
;      REFERENCE/DOCKET NUMBER:  4105/136-00
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (201) 235-4387
;      TELEFAX:  (201) 235-3500
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;      TISSUE TYPE:  Blood
;      CELL TYPE:  Macrophage
US-08-397-470-1

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 7
US-08-192-102-1
; Sequence 1, Application US/08192102
; Patent No. 5656272
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES AND ASSAYS EMPLOYING
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,102
;      FILING DATE:  04-FEB-1994
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,093
;      FILING DATE:  04-FEB-1994
;      APPLICATION NUMBER:  US 08/013,413
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/010,406
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,852
;      FILING DATE:  11-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,606
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/670,827
;      FILING DATE:  18-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
```

```
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  NYU93-01M3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-192-102-1

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 8
US-08-324-799-1
; Sequence 1, Application US/08324799
; Patent No. 5698195
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  ANTI-TNF ANTIBODIES AND PEPTIDES
;    TITLE OF INVENTION:  OF HUMAN TUMOR NECROSIS FACTOR
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/324,799
;      FILING DATE:  18-OCT-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,093
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,102
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/192,861
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/013,413
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/010,406
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,852
;      FILING DATE:  11-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,606
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/670,827
;      FILING DATE:  18-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  NYU93-01M4
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (617) 861-6240
;      TELEFAX:  (617) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-324-799-1

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||| |||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 9
US-08-538-875-1
; Sequence 1, Application US/08538875
; Patent No. 5773582
;  GENERAL INFORMATION:
;    APPLICANT:  Shin, Hang-Cheol
;    APPLICANT:  Shin, Nam-Kyu
;    APPLICANT:  Lee, Inkyung
;    APPLICANT:  Kang, Sungzong
;    TITLE OF INVENTION:  TUMOR NECROSIS FACTOR MUTEINS
;    NUMBER OF SEQUENCES:  73
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Shin, Hang-Cheol
;      STREET:  Jukong Gocheung Apt. 1014-806, Haan-dong
;      CITY:  Kwangmyung-shi
;      STATE:  Kyungki-do
;      COUNTRY:  Republic of Korea
;      ZIP:  423-060
;      ADDRESSEE:  Shin, Nam-Kyu
;      STREET:  #181-404 Sadang-4-dong, Dongjak-ku
;      CITY:  Seoul
;      STATE:
;      COUNTRY:  Republic of Korea
;      ZIP:  156-094
;      ADDRESSEE:  Lee, Inkyung
;      STREET:  11/2, #302-39 Juan-4-dong, Nam-ku
;      CITY:  Incheon
;      STATE:
;      COUNTRY:  Republic of Korea
;      ZIP:  402-204
```

```
;      ADDRESSEE:  Kang, Sungzong
;      STREET:  #84-4 Daeshin-dong, Seodaemun-ku
;      CITY:  Seoul
;      STATE:
;      COUNTRY:  Republic of Korea
;      ZIP:  120-160
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette 3.5inch 2.0Mb storage
;      COMPUTER:  IBM PC/AT
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WordPerfect 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/538,875
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/193,336
;      FILING DATE:
;      APPLICATION NUMBER:  KR 93-1751
;      FILING DATE:  9-FEB-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:
;      REGISTRATION NUMBER:
;      REFERENCE/DOCKET NUMBER:
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:
;      TELEFAX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-538-875-1

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 10
US-08-394-600B-17
; Sequence 17, Application US/08394600B
; Patent No. 5843693
;  GENERAL INFORMATION:
;    APPLICANT:  Halenbeck, Robert F.
;    APPLICANT:  Jewell, David A.
;    APPLICANT:  Koths, Kirston E.
;    APPLICANT:  Kriegler, Michael
;    APPLICANT:  Perez, Carl
;    TITLE OF INVENTION:  Compositions for the Inhibition of
;    TITLE OF INVENTION:  Protein Hormone Formation and Uses Thereof
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  McAndrews, Held & Malloy, Ltd.
;      STREET:  500 West Madison Street; 34th Floor
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60661
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/394,600B
;      FILING DATE:  02/27/95
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Donald J. Pochopien
;      REGISTRATION NUMBER:  32,167
;      REFERENCE/DOCKET NUMBER:  820.005/11850US05
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/707-8889
;      TELEFAX:  312/707-9155
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  17:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-394-600B-17

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 11
US-08-500-860A-35
; Sequence 35, Application US/08500860A
; Patent No. 5891679
;  GENERAL INFORMATION:
;    APPLICANT:  LUCAS, RUDOLPH
;    APPLICANT:  DE BAETSELIER, PATRICK
;    APPLICANT:  FRANSEN, LUCIE
;    APPLICANT:  SABLON, ERWIN
;    TITLE OF INVENTION:  TNF-MUTEINS, A PROCESS FOR PREPARING THEM AND
;    TITLE OF INVENTION:  THEIR USE AS ACTIVE SUBSTANCES IN PHARMACEUTICAL COMPOSITIONS
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  NIXON & VANDERHYE P.C.
;      STREET:  1100 NORTH GLEBE ROAD
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  U.S.A.
;      ZIP:  22201-4714
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/500,860A
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  BYRNE, THOMAS E.
;      REGISTRATION NUMBER:  32,205
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;      REFERENCE/DOCKET NUMBER:  1487-8
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703)816-4000
;      TELEFAX:  (703)816-4100
;      TELEX:  200797 NIXN UR
;  INFORMATION FOR SEQ ID NO:  35:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-500-860A-35

  Query Match            99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 12
US-08-192-861A-1
; Sequence 1, Application US/08192861A
; Patent No. 5919452
;  GENERAL INFORMATION:
;    APPLICANT:  Le, Junming
;    APPLICANT:  Vilcek, Jan
;    APPLICANT:  Daddona, Peter E.
;    APPLICANT:  Ghrayeb, John
;    APPLICANT:  Knight, David M.
;    APPLICANT:  Siegel, Scott A.
;    TITLE OF INVENTION:  METHODS OF TREATING TNF'-MEDIATED DISEASE USING
;    TITLE OF INVENTION:  CHIMERIC ANTI-TNF ANTIBODIES (As Amended)
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Hamilton, Brook, Smith & Reynolds, P.C.
;      STREET:  Two Militia Drive
;      CITY:  Lexington
;      STATE:  Massachusetts
;      COUNTRY:  USA
;      ZIP:  02173
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/192,861A
;      FILING DATE:  04-FEB-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/013,413
;      FILING DATE:  02-FEB-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/010,406
;      FILING DATE:  29-JAN-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/943,852
;      FILING DATE:  11-SEP-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,606
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/670,827
;      FILING DATE:  18-MAR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Brook, David E.
;      REGISTRATION NUMBER:  22,592
;      REFERENCE/DOCKET NUMBER:  NYU93-01M2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (781) 861-6240
;      TELEFAX:  (781) 861-9540
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-192-861A-1

  Query Match            99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 13
US-08-600-783-5
; Sequence 5, Application US/08600783
; Patent No. 5962267
;  GENERAL INFORMATION:
;    APPLICANT:  SHIN, Hang Cheol
;    APPLICANT:  CHANG, Seung Gu
;    APPLICANT:  KIM, Dae Young
;    APPLICANT:  KIM, Chong Suhl
;    TITLE OF INVENTION:  Proinsulin Derivative and Process
;    TITLE OF INVENTION:  for Producing Human Insulin
;    NUMBER OF SEQUENCES:  36
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SHIN, Hang Cheol
;      STREET:  Ssangma-Hanshin Apt. 102-1206,
;      STREET:  #245 Cholsan-dong
;      CITY:  Kwangmyung-shi
;      STATE:  Kyungki-do
;      COUNTRY:  Republic of Korea
;      ZIP:  423-030
;      ADDRESSEE:  CHANG, Seung Gu
;      STREET:  Hyundai Apt. 71-203, Apkujong-dong,
;      STREET:  Kangnam-ku
;      CITY:  Seoul
;      STATE:  Seoul
;      COUNTRY:  Republic of Korea
;      ZIP:  135-110
;      ADDRESSEE:  KIM, Dae Young
;      STREET:  Sosa Jukong Apt. 108-202, Sosa Bon-dong,
;      STREET:  Sosa-ku
;      CITY:  Bucheon-shi
;      STATE:  Kyungki-do
;      COUNTRY:  Republic of Korea
;      ZIP:  422-230
;      ADDRESSEE:  KIM, Chong Suhl
;      STREET:  Garden Heights Apt. 202-801, #100,
;      STREET:  Hwangkeum-dong, Soosung-ku
;      CITY:  Taegu
;      STATE:  Taegu
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;       COUNTRY:  Republic of Korea
;       ZIP:  706-040
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy Disk, 3.5 inch, 1.44MB storage
;       COMPUTER:  IBM PC/AT
;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  Word Perfect 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/600,783
;       FILING DATE:
;       CLASSIFICATION:  514
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  KR 95-2751
;       FILING DATE:  15-FEB-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Shahan Islam
;       REGISTRATION NUMBER:  32,507
;       REFERENCE/DOCKET NUMBER:
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (212) 278-1000
;       TELEFAX:  (212) 953-7249
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  157 amino acids
;       TYPE:  amino acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-600-783-5

  Query Match             99.2%;  Score 774;  DB 1;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 14
US-08-584-031-13
; Sequence 13, Application US/08584031A
; Patent No. 6030945
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  TITLE OF INVENTION: APO-2 LIGAND
;  FILE REFERENCE: 11669.22US03
;  CURRENT APPLICATION NUMBER: US/08/584,031A
;  CURRENT FILING DATE: 1996-01-09
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-08-584-031-13

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 15
US-08-714-960B-1
; Sequence 1, Application US/08714960B
; Patent No. 6121237
;  GENERAL INFORMATION:
;    APPLICANT:  RATHJEN, Deborah A
;    APPLICANT:  FERRANTE, Antonio
;    TITLE OF INVENTION:  Neutrophil Stimulating Peptides
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  BANNER & WITCOFF, LTD.
;      STREET:  10 S. Wacker Drive, Suite 3000
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60606
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  1.44 Mb storage diskette, 3.50 inch
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  IBM compatible PC/MS-DOS
;      SOFTWARE:  WordPerfect version 6.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,960B
;      FILING DATE:  17-SEP-1996
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  AU PJ9065
;      FILING DATE:  12-MAR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/AU91/00086
;      FILING DATE:  12-MAR-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/930,415
;      FILING DATE:  09-NOV-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/107,235
;      FILING DATE:  16-AUG-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Resis, Robert H.
;      REGISTRATION NUMBER:  32,168
;      REFERENCE/DOCKET NUMBER:  92,622-B
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 715-1000
;      TELEFAX:  (312) 715-1234
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  157 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  not relevant
;    MOLECULE TYPE:  protein
;    FEATURE:
;      NAME/KEY:  Protein
;      LOCATION:  1..157
;      OTHER INFORMATION:  /note= "Human TNF"
US-08-714-960B-1

  Query Match             99.2%;  Score 774;  DB 2;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 1.1e-78;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Search completed: April 3, 2006, 08:22:00
Job time : 23 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-668-178-2
Perfect score: 780
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 180808

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_New:*
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2: /SIDS5/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /SIDS5/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	774	99.2	157	7	US-11-053-750-1	Sequence 1, Appli
3	774	99.2	157	7	US-11-053-749-1	Sequence 1, Appli
4	774	99.2	157	7	US-11-108-001-12	Sequence 12, Appl
5	774	99.2	157	7	US-11-170-753-1	Sequence 1, Appli
6	774	99.2	157	7	US-11-179-359-1	Sequence 1, Appli
7	774	99.2	157	7	US-11-181-030-1	Sequence 1, Appli
8	774	99.2	157	7	US-11-182-033-1	Sequence 1, Appli
9	774	99.2	157	7	US-11-195-589-1	Sequence 1, Appli
10	774	99.2	158	7	US-11-082-544-4	Sequence 4, Appli
11	774	99.2	164	7	US-11-108-001-2	Sequence 2, Appli
12	774	99.2	180	7	US-11-082-544-8	Sequence 8, Appli
13	765	98.1	157	6	US-10-504-389A-55	Sequence 55, Appl
14	629.5	80.7	235	7	US-11-032-797-8	Sequence 8, Appli
15	486	62.3	104	7	US-11-065-669-5	Sequence 5, Appli
16	209.5	26.9	177	6	US-10-999-866-61	Sequence 61, Appl
17	209.5	26.9	205	6	US-10-995-561-1028	Sequence 1028, Ap
18	209.5	26.9	205	6	US-10-995-561-1029	Sequence 1029, Ap
19	168.5	21.6	204	7	US-11-136-341A-31	Sequence 31, Appl
20	168.5	21.6	240	7	US-11-136-341A-1	Sequence 1, Appli
21	166.5	21.3	179	6	US-10-861-934-14	Sequence 14, Appl
22	166.5	21.3	240	6	US-10-987-663-6	Sequence 6, Appli
23	166.5	21.3	278	6	US-10-861-934-16	Sequence 16, Appl
24	166.5	21.3	278	6	US-10-861-934-26	Sequence 26, Appl
25	161.5	20.7	137	6	US-10-861-934-10	Sequence 10, Appl
26	161.5	20.7	138	6	US-10-861-934-12	Sequence 12, Appl
27	160.5	20.6	179	6	US-10-861-934-22	Sequence 22, Appl
28	160.5	20.6	279	6	US-10-861-934-24	Sequence 24, Appl
29	160.5	20.6	279	6	US-10-861-934-32	Sequence 32, Appl
30	160.5	20.6	279	7	US-11-032-797-5	Sequence 5, Appli
31	156.5	20.1	137	6	US-10-861-934-18	Sequence 18, Appl
32	156.5	20.1	138	6	US-10-861-934-20	Sequence 20, Appl
33	153	19.6	239	7	US-11-136-341A-2	Sequence 2, Appli
34	152	19.5	359	7	US-11-105-172-2	Sequence 2, Appli
35	151	19.4	179	6	US-10-861-934-6	Sequence 6, Appli
36	151	19.4	239	7	US-11-136-341A-3	Sequence 3, Appli
37	151	19.4	281	6	US-10-861-934-8	Sequence 8, Appli
38	151	19.4	281	6	US-10-861-934-30	Sequence 30, Appl
39	151	19.4	281	7	US-11-213-368-11	Sequence 11, Appl
40	151	19.4	281	7	US-11-213-368-12	Sequence 12, Appl
41	150.5	19.3	242	7	US-11-136-341A-25	Sequence 25, Appl
42	149.5	19.2	136	6	US-10-861-934-83	Sequence 83, Appl
43	149.5	19.2	137	6	US-10-861-934-2	Sequence 2, Appli
44	149.5	19.2	137	6	US-10-861-934-82	Sequence 82, Appl
45	149.5	19.2	138	6	US-10-861-934-4	Sequence 4, Appli
46	149.5	19.2	138	6	US-10-861-934-81	Sequence 81, Appl
47	149.5	19.2	139	6	US-10-861-934-80	Sequence 80, Appl
48	149.5	19.2	141	6	US-10-861-934-79	Sequence 79, Appl
49	149	19.1	178	6	US-10-861-934-84	Sequence 84, Appl
50	148.5	19.0	204	7	US-11-136-341A-32	Sequence 32, Appl
51	143	18.3	130	6	US-10-861-934-28	Sequence 28, Appl
52	139	17.8	306	7	US-11-032-797-7	Sequence 7, Appli
53	120	15.4	316	7	US-11-032-797-4	Sequence 4, Appli
54	120	15.4	316	7	US-11-238-266-2	Sequence 2, Appli
55	119.5	15.3	291	7	US-11-032-797-6	Sequence 6, Appli
56	116	14.9	317	7	US-11-136-079-2	Sequence 2, Appli
57	113	14.5	102	7	US-11-065-669-7	Sequence 7, Appli
58	113	14.5	261	7	US-11-136-079-4	Sequence 4, Appli
59	112	14.4	245	7	US-11-032-797-2	Sequence 2, Appli
60	104.5	13.4	266	7	US-11-082-544-10	Sequence 10, Appl
61	104.5	13.4	281	6	US-10-821-234-1288	Sequence 1288, Ap
62	104.5	13.4	281	6	US-10-501-035-269	Sequence 269, App
63	104.5	13.4	281	7	US-11-077-272-2	Sequence 2, Appli
64	104.5	13.4	281	7	US-11-136-842-1	Sequence 1, Appli
65	104.5	13.4	281	7	US-11-136-079-5	Sequence 5, Appli
66	104.5	13.4	281	7	US-11-221-281-5	Sequence 5, Appli
67	104.5	13.4	391	7	US-11-105-172-4	Sequence 4, Appli
68	97.5	12.5	136	7	US-11-084-647-11	Sequence 11, Appl
69	97.5	12.5	250	6	US-10-742-634-11	Sequence 11, Appl
70	97.5	12.5	250	7	US-11-054-515-3239	Sequence 3239, Ap
71	97.5	12.5	250	7	US-11-084-647-6	Sequence 6, Appli
72	97.5	12.5	250	7	US-11-136-079-3	Sequence 3, Appli
73	97.5	12.5	250	7	US-11-242-294-4	Sequence 4, Appli
74	97.5	12.5	250	7	US-11-266-444-3239	Sequence 3239, Ap
75	93	11.9	188	7	US-11-054-515-3235	Sequence 3235, Ap
76	93	11.9	188	7	US-11-266-444-3235	Sequence 3235, Ap
77	93	11.9	266	7	US-11-054-515-3229	Sequence 3229, Ap
78	93	11.9	266	7	US-11-266-444-3229	Sequence 3229, Ap
79	92.5	11.9	135	7	US-11-084-647-4	Sequence 4, Appli
80	92.5	11.9	220	7	US-11-054-515-3233	Sequence 3233, Ap
81	92.5	11.9	220	7	US-11-266-444-3233	Sequence 3233, Ap
82	92.5	11.9	239	7	US-11-054-515-3232	Sequence 3232, Ap
83	92.5	11.9	239	7	US-11-266-444-3232	Sequence 3232, Ap
84	91.5	11.7	207	7	US-11-054-515-3234	Sequence 3234, Ap
85	91.5	11.7	207	7	US-11-266-444-3234	Sequence 3234, Ap
86	91.5	11.7	241	7	US-11-084-647-5	Sequence 5, Appli
87	91.5	11.7	290	7	US-11-054-515-3231	Sequence 3231, Ap
88	91.5	11.7	290	7	US-11-266-444-3231	Sequence 3231, Ap
89	91.5	11.7	309	7	US-11-065-669-2	Sequence 2, Appli
90	91.5	11.7	309	7	US-11-054-515-3230	Sequence 3230, Ap
91	91.5	11.7	309	7	US-11-187-364-17	Sequence 17, Appl
92	91.5	11.7	309	7	US-11-266-444-3230	Sequence 3230, Ap
93	88.5	11.3	152	6	US-10-742-634-3	Sequence 3, Appli
94	88.5	11.3	178	6	US-10-742-634-17	Sequence 17, Appl
95	88.5	11.3	219	7	US-11-054-515-3237	Sequence 3237, Ap
96	88.5	11.3	219	7	US-11-266-444-3237	Sequence 3237, Ap
97	88.5	11.3	243	7	US-11-054-515-3236	Sequence 3236, Ap
98	88.5	11.3	243	7	US-11-266-444-3236	Sequence 3236, Ap

99	88.5	11.3	285	6	US-10-131-826A-24	Sequence 24, Appl
100	88.5	11.3	285	6	US-10-742-634-2	Sequence 2, Appli

ALIGNMENTS

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RESULT 1
US-11-010-954-1
; Sequence 1, Application US/11010954
; Publication No. US20050249735A1
; GENERAL INFORMATION:
; APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  APPLICANT:  Shealy, David
;  TITLE OF INVENTION: Methods of Treating Ankylosing Spondylitis Using Anti-TNF Antibod
;  TITLE OF INVENTION:  and Peptides of Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-043
;  CURRENT APPLICATION NUMBER: US/11/010,954
;  CURRENT FILING DATE:  2004-12-13
;  PRIOR APPLICATION NUMBER: US 10/637,759
;  PRIOR FILING DATE: 2003-08-08
;  PRIOR APPLICATION NUMBER: US 09/920,137
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: US 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: US 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: US 60/236,826
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: US 60/223,360
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-010-954-1

  Query Match             99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 2
US-11-053-750-1
; Sequence 1, Application US/11053750
; Publication No. US20050255104A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  APPLICANT:  Scallon, Bernard
;  TITLE OF INVENTION: Methods of Treating Psoriasis Using
;  TITLE OF INVENTION:  Anti-TNF Receptor Fusion Proteins
;  FILE REFERENCE: 0975.1005-045
;  CURRENT APPLICATION NUMBER: US/11/053,750
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: U.S. 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 09/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-053-750-1

  Query Match             99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 3
US-11-053-749-1
; Sequence 1, Application US/11053749
; Publication No. US20050260201A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  APPLICANT:  Scallon, Bernard
;  TITLE OF INVENTION: Methods of Treating Rheumatoid Arthritis
;  TITLE OF INVENTION:  Using Anti-TNF Receptor Fusion Proteins
;  FILE REFERENCE: 0975.1005-040
;  CURRENT APPLICATION NUMBER: US/11/053,749
;  CURRENT FILING DATE:  2005-02-07
;  PRIOR APPLICATION NUMBER: US/09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
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;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S.08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-053-749-1

  Query Match            99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 4
US-11-108-001-12
; Sequence 12, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Steed, Paul Michael
;  APPLICANT:  Zalevsky, Jonathan
;  APPLICANT:  Szymkowski, David Edmund
;  TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
;  TITLE OF INVENTION:  RELATED DISORDERS
;  FILE REFERENCE: A-68990-7
;  CURRENT APPLICATION NUMBER: US/11/108,001
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US 10/963,994
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: US 09/798,789
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: US 09/945,150
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 09/981,289
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: US 10/262,630
;  PRIOR FILING DATE: 2002-09-30
;  PRIOR APPLICATION NUMBER: US 60/553,908
;  PRIOR FILING DATE: 2004-03-17
;  PRIOR APPLICATION NUMBER: US 60/510,430
;  PRIOR FILING DATE: 2003-10-10
;  PRIOR APPLICATION NUMBER: US 60/509,960
;  PRIOR FILING DATE: 2003-10-09
;  PRIOR APPLICATION NUMBER: US 60/528,275
;  PRIOR FILING DATE: 2003-12-08
;  PRIOR APPLICATION NUMBER: US 60/523,647
;  PRIOR FILING DATE: 2003-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-108-001-12

  Query Match            99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 5
US-11-170-753-1
; Sequence 1, Application US/11170753
; Publication No. US20060013816A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Methods of Treating Psoriasis Using
;  TITLE OF INVENTION:  Human Anti-TNF Antibodies and Fragments
;  FILE REFERENCE: 0975.1005-050
;  CURRENT APPLICATION NUMBER: US/11/170,753
;  CURRENT FILING DATE:  2005-06-29
;  PRIOR APPLICATION NUMBER: U.S. 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S.08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-170-753-1

  Query Match            99.2%;  Score 774;  DB 7;  Length 157;
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  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 6
US-11-179-359-1
; Sequence 1, Application US/11179359
; Publication No. US20060018905A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Methods for Treating Systemic Lupus Erythematosus
;  TITLE OF INVENTION:  Using Anti-TNF Antibodies and Fragments Thereof
;  FILE REFERENCE: 0975.1005-054
;  CURRENT APPLICATION NUMBER: US/11/179,359
;  CURRENT FILING DATE:  2005-07-12
;  PRIOR APPLICATION NUMBER: U.S. 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S.08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-179-359-1

  Query Match             99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 7
US-11-181-030-1
; Sequence 1, Application US/11181030
; Publication No. US20060018906A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Methods for Treating Sarcoidosis Using
;  TITLE OF INVENTION:  Anti-TNF Antibodies and Fragments Thereof
;  FILE REFERENCE: 0975.1005-055
;  CURRENT APPLICATION NUMBER: US/11/181,030
;  CURRENT FILING DATE:  2005-07-13
;  PRIOR APPLICATION NUMBER: U.S. 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S.08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-181-030-1

  Query Match             99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 8
US-11-182-033-1
; Sequence 1, Application US/11182033
; Publication No. US20060018907A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
```

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;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  APPLICANT:  Shealy, David
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of Human
;  TITLE OF INVENTION:  Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-044
;  CURRENT APPLICATION NUMBER: US/11/182,033
;  CURRENT FILING DATE:  2005-07-14
;  PRIOR APPLICATION NUMBER: US 10/637,759
;  PRIOR FILING DATE: 2003-08-08
;  PRIOR APPLICATION NUMBER: US 09/920,137
;  PRIOR FILING DATE: 2001-08-01
;  PRIOR APPLICATION NUMBER: US 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: US 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: US 60/236,826
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: US 60/223,360
;  PRIOR FILING DATE: 2000-08-07
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-182-033-1

  Query Match             99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 9
US-11-195-589-1
; Sequence 1, Application US/11195589
; Publication No. US20060024310A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Methods of Treating TNFa-Mediated
;  TITLE OF INVENTION:  Tissue Injury Using Anti-TNF Antibodies and Peptides
;  FILE REFERENCE: 0975.1005-042
;  CURRENT APPLICATION NUMBER: US/11/195,589
;  CURRENT FILING DATE:  2005-08-02
;  PRIOR APPLICATION NUMBER: US 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: US 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: US 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: US 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: US 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: US 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: US 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: US 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: US 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: US 08/013,413
;  PRIOR FILING DATE: 02-02-1993
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 30
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-195-589-1

  Query Match             99.2%;  Score 774;  DB 7;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 10
US-11-082-544-4
; Sequence 4, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
;  APPLICANT: Bermudes, G.
;  APPLICANT:  King, I.
;  APPLICANT:  Clairmont, C.
;  APPLICANT:  Lin, S.
;  APPLICANT:  Belcourt, M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
;  FILE REFERENCE: 8002-059
;  CURRENT APPLICATION NUMBER: US/11/082,544
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: US/09/645,415
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: 60/157,581
;  PRIOR FILING DATE: 1999-10-04
;  PRIOR APPLICATION NUMBER: 60/157,637
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 4
;   LENGTH: 158
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-082-544-4

  Query Match             99.2%;  Score 774;  DB 7;  Length 158;
  Best Local Similarity   96.2%;  Pred. No. 2.4e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 61
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```
Qy          61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
               |||| |||||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db          62 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 121

Qy         121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               ||||||| ||||||||||||||||||||||||||||
Db         122 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 158
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RESULT 11
US-11-108-001-2
; Sequence 2, Application US/11108001
; Publication No. US20050265962A1
; GENERAL INFORMATION:
;  APPLICANT: Desjarlais, John R.
;  APPLICANT:  Steed, Paul Michael
;  APPLICANT:  Zalevsky, Jonathan
;  APPLICANT:  Szymkowski, David Edmund
;  TITLE OF INVENTION: PROTEIN BASED TNF-ALPHA VARIANTS FOR THE TREATMENT OF TNF-ALPHA
;  TITLE OF INVENTION:  RELATED DISORDERS
;  FILE REFERENCE: A-68990-7
;  CURRENT APPLICATION NUMBER: US/11/108,001
;  CURRENT FILING DATE:  2005-04-14
;  PRIOR APPLICATION NUMBER: US 10/963,994
;  PRIOR FILING DATE: 2004-10-12
;  PRIOR APPLICATION NUMBER: US 09/798,789
;  PRIOR FILING DATE: 2001-03-02
;  PRIOR APPLICATION NUMBER: US 09/945,150
;  PRIOR FILING DATE: 2001-08-31
;  PRIOR APPLICATION NUMBER: US 09/981,289
;  PRIOR FILING DATE: 2001-10-15
;  PRIOR APPLICATION NUMBER: US 10/262,630
;  PRIOR FILING DATE: 2002-09-30
;  PRIOR APPLICATION NUMBER: US 60/553,908
;  PRIOR FILING DATE: 2004-03-17
;  PRIOR APPLICATION NUMBER: US 60/510,430
;  PRIOR FILING DATE: 2003-10-10
;  PRIOR APPLICATION NUMBER: US 60/509,960
;  PRIOR FILING DATE: 2003-10-09
;  PRIOR APPLICATION NUMBER: US 60/528,275
;  PRIOR FILING DATE: 2003-12-08
;  PRIOR APPLICATION NUMBER: US 60/523,647
;  PRIOR FILING DATE: 2003-11-20
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 13
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
;   LENGTH: 164
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-108-001-2

  Query Match             99.2%;  Score 774;  DB 7;  Length 164;
  Best Local Similarity   96.2%;  Pred. No. 2.5e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy           1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db           8 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 67

Qy          61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
               |||| |||||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db          68 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 127

Qy         121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               ||||||| ||||||||||||||||||||||||||||
Db         128 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 164


RESULT 12
US-11-082-544-8
; Sequence 8, Application US/11082544
; Publication No. US20050249706A1
; GENERAL INFORMATION:
;  APPLICANT: Bermudes, G.
;  APPLICANT:  King, I.
;  APPLICANT:  Clairmont, C.
;  APPLICANT:  Lin, S.
;  APPLICANT:  Belcourt, M.
;  TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
;  FILE REFERENCE: 8002-059
;  CURRENT APPLICATION NUMBER: US/11/082,544
;  CURRENT FILING DATE:  2005-03-17
;  PRIOR APPLICATION NUMBER: US/09/645,415
;  PRIOR FILING DATE: 2000-08-24
;  PRIOR APPLICATION NUMBER: 60/157,581
;  PRIOR FILING DATE: 1999-10-04
;  PRIOR APPLICATION NUMBER: 60/157,637
;  PRIOR FILING DATE: 1999-10-04
;  NUMBER OF SEQ ID NOS: 61
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 8
;   LENGTH: 180
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Fusion construct
US-11-082-544-8

  Query Match             99.2%;  Score 774;  DB 7;  Length 180;
  Best Local Similarity   96.2%;  Pred. No. 2.8e-86;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy           1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
               |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db          24 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 83

Qy          61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
               |||| |||||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db          84 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 143

Qy         121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               ||||||| ||||||||||||||||||||||||||||
Db         144 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 180


RESULT 13
US-10-504-389A-55
; Sequence 55, Application US/10504389A
; Publication No. US20060045876A1
; GENERAL INFORMATION:
;  APPLICANT: Renner, Christoph
;  APPLICANT:  Scott, Andrew
;  TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
;  TITLE OF INVENTION:  ANTIBODIES AND USES THEREOF
;  FILE REFERENCE: LUD 5821
;  CURRENT APPLICATION NUMBER: US/10/504,389A
;  CURRENT FILING DATE:  2004-08-10
;  PRIOR APPLICATION NUMBER: PCT/US03/04243
;  PRIOR FILING DATE: 2002-02-12
;  NUMBER OF SEQ ID NOS: 56
; SEQ ID NO 55
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: amino acid sequence of a TNF fragment
US-10-504-389A-55

  Query Match             98.1%;  Score 765;  DB 6;  Length 157;
  Best Local Similarity   96.1%;  Pred. No. 2.9e-85;
  Matches  149;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy           3 SSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 62
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                ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 SSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 62

Qy         63 LFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGG 122
               || |||||||||||||||||||||||| ||||||| |||||||||||||| ||||||||||
Db         63 LFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGG 122

Qy        123 VFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
               ||||| ||||||||||||||||||||||||||||||
Db        123 VFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 14
US-11-032-797-8
; Sequence 8, Application US/11032797
; Publication No. US20050287545A1
;  GENERAL INFORMATION:
;    APPLICANT:  Choi, Yongwon
;    APPLICANT:  Wong, Brian
;    APPLICANT:  Josien, Regis
;    APPLICANT:  Steinman, Ralph
;    TITLE OF INVENTION:  A PROTEIN BELONGING TO THE TNF  SUPERFAMILY
;    TITLE OF INVENTION:  INVOLVED IN SIGNAL TRANSDUCTION, NUCLEIC ACIDS ENCODING SAME,
;    TITLE OF INVENTION:  METHODS OF USE THEREOF
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Klauber & Jackson
;      STREET:  411 Hackensack Avenue, 4th Floor
;      CITY:  Hackensack
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07601
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/11/032,797
;      FILING DATE:  11-JAN-2005
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/873,829
;      FILING DATE:  04-Jun-2001
;      APPLICATION NUMBER:  09/210,115
;      FILING DATE:  <Unknown>
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Jackson Esq., David A.
;      REGISTRATION NUMBER:  26,742
;      REFERENCE/DOCKET NUMBER:  600-1-200 CIP N
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-487-5800
;      TELEFAX:  201-343-1684
;      TELEX:  133521
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  235 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
;    HYPOTHETICAL:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Mus musculus
US-11-032-797-8

  Query Match            80.7%;  Score 629.5;  DB 7;  Length 235;
  Best Local Similarity  75.2%;  Pred. No. 1.3e-68;
  Matches  118;  Conservative   20;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| | | ||:||::|||||||||::|:|||||||::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| ||||| :|||||:|| |:||| |||||: ||| ::|||||  ||||||||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||:||||:| | ||||||||||||||:|||
Db        199 GGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 15
US-11-065-669-5
; Sequence 5, Application US/11065669
; Publication No. US20050244411A1
; GENERAL INFORMATION:
;  APPLICANT: MacKay, Fabienne
;  APPLICANT:  Kalled, Susan
;  TITLE OF INVENTION: BAFF, INHIBITORS THEREOF AND THEIR USE IN THE
;  TITLE OF INVENTION:  MODULATION OF B-CELL RESPONSE
;  FILE REFERENCE: 08201.0024-04000
;  CURRENT APPLICATION NUMBER: US/11/065,669
;  CURRENT FILING DATE:  2005-02-24
;  PRIOR APPLICATION NUMBER: 10/045,574
;  PRIOR FILING DATE: 2001-11-07
;  PRIOR APPLICATION NUMBER: 09/911,777
;  PRIOR FILING DATE: 2001-07-24
;  PRIOR APPLICATION NUMBER: 60/143,228
;  PRIOR FILING DATE: 2001-07-09
;  PRIOR APPLICATION NUMBER: PCT/US00/01788
;  PRIOR FILING DATE: 2000-01-25
;  PRIOR APPLICATION NUMBER: 60/117,169
;  PRIOR FILING DATE: 1999-01-25
;  NUMBER OF SEQ ID NOS: 26
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 104
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-11-065-669-5

  Query Match            62.3%;  Score 486;  DB 7;  Length 104;
  Best Local Similarity  72.5%;  Pred. No. 1.2e-51;
  Matches  100;  Conservative    0;  Mismatches    4;  Indels   34;  Gaps    2;

Qy          9 SDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQG 68
              || |||||||||||||||||||||||||||||||||||||||||||||||||| |||||| |||
Db          1 SDKPVAHVVANPQAEGQLQWLNRRANALLANGV----------------YSQVLFKGQG 43

Qy         69 CPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLEX 128
              |||||||||||||||||||||||                ||||| ||||||||||||||
Db         44 CPSTHVLLTHTISRIAVSYQT----------------EGAEAKPWYEPIYLGGVFQLEK 86

Qy        129 GDRLSAEINRPDYLDFAE 146
              ||||||||||||||||||
Db         87 GDRLSAEINRPDYLDFAE 104


Search completed: April  3, 2006, 08:22:44
Job time : 12 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:22:16 ; Search time 50 Seconds
(without alignments)
1311.984 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 780
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published_Applications_AA_Main:*
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	778	99.7	157	5	US-10-668-178-15	Sequence 15, Appl
2	778	99.7	157	5	US-10-668-178-16	Sequence 16, Appl
3	774	99.2	157	3	US-09-756-301A-1	Sequence 1, Appli
4	774	99.2	157	3	US-09-927-703-1	Sequence 1, Appli
5	774	99.2	157	3	US-09-854-280-19	Sequence 19, Appl
6	774	99.2	157	3	US-09-934-465-13	Sequence 13, Appl
7	774	99.2	157	3	US-09-766-535A-1	Sequence 1, Appli
8	774	99.2	157	3	US-09-854-208-19	Sequence 19, Appl
9	774	99.2	157	3	US-09-756-161A-1	Sequence 1, Appli
10	774	99.2	157	3	US-09-903-327A-7	Sequence 7, Appli
11	774	99.2	157	3	US-09-756-398B-1	Sequence 1, Appli
12	774	99.2	157	3	US-09-897-724-1	Sequence 1, Appli
13	774	99.2	157	4	US-10-010-229-1	Sequence 1, Appli
14	774	99.2	157	4	US-10-043-450-1	Sequence 1, Appli
15	774	99.2	157	4	US-10-044-534-1	Sequence 1, Appli
16	774	99.2	157	4	US-10-099-007A-1	Sequence 1, Appli
17	774	99.2	157	4	US-10-043-432-1	Sequence 1, Appli
18	774	99.2	157	4	US-10-119-621-1	Sequence 1, Appli
19	774	99.2	157	4	US-10-208-145-1	Sequence 1, Appli
20	774	99.2	157	4	US-10-262-630-9	Sequence 9, Appli
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22	774	99.2	157	4	US-10-305-347A-9	Sequence 9, Appli
23	774	99.2	157	4	US-10-198-845-1	Sequence 1, Appli
24	774	99.2	157	4	US-10-227-488-1	Sequence 1, Appli
25	774	99.2	157	4	US-10-170-812-7	Sequence 7, Appli
26	774	99.2	157	4	US-10-187-121-1	Sequence 1, Appli
27	774	99.2	157	4	US-10-176-460-1	Sequence 1, Appli
28	774	99.2	157	4	US-10-186-559-1	Sequence 1, Appli
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30	774	99.2	157	4	US-10-200-795-1	Sequence 1, Appli
31	774	99.2	157	4	US-10-319-011-1	Sequence 1, Appli
32	774	99.2	157	4	US-10-371-443-1	Sequence 1, Appli
33	774	99.2	157	4	US-10-379-866-1	Sequence 1, Appli
34	774	99.2	157	4	US-10-371-962-1	Sequence 1, Appli
35	774	99.2	157	4	US-10-354-985-1	Sequence 1, Appli
36	774	99.2	157	4	US-10-354-985-2	Sequence 2, Appli
37	774	99.2	157	4	US-10-397-786A-1	Sequence 1, Appli
38	774	99.2	157	4	US-10-665-971-1	Sequence 1, Appli
39	774	99.2	157	4	US-10-637-759-1	Sequence 1, Appli
40	774	99.2	157	4	US-10-327-619-1	Sequence 1, Appli
41	774	99.2	157	4	US-10-774-118-1	Sequence 1, Appli
42	774	99.2	157	4	US-10-394-471B-17	Sequence 17, Appl
43	774	99.2	157	5	US-10-861-685-13	Sequence 13, Appl
44	774	99.2	157	5	US-10-668-178-1	Sequence 1, Appli
45	774	99.2	157	5	US-10-668-178-2	Sequence 2, Appli
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47	774	99.2	157	5	US-10-727-155-265	Sequence 265, App
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49	774	99.2	157	5	US-10-652-979-13	Sequence 13, Appl
50	774	99.2	157	5	US-10-954-900A-9	Sequence 9, Appli
51	774	99.2	158	4	US-10-295-074-17	Sequence 17, Appl
52	774	99.2	158	5	US-10-738-423-4	Sequence 4, Appli
53	774	99.2	158	5	US-10-846-911-17	Sequence 17, Appl
54	774	99.2	158	5	US-10-939-107-17	Sequence 17, Appl
55	774	99.2	164	3	US-09-798-789-2	Sequence 2, Appli
56	774	99.2	164	3	US-09-981-289-2	Sequence 2, Appli
57	774	99.2	164	5	US-10-963-994-2	Sequence 2, Appli
58	774	99.2	173	4	US-10-295-074-28	Sequence 28, Appl
59	774	99.2	173	5	US-10-846-911-28	Sequence 28, Appl
60	774	99.2	173	5	US-10-939-107-28	Sequence 28, Appl
61	774	99.2	180	5	US-10-738-423-8	Sequence 8, Appli
62	774	99.2	193	3	US-09-982-308-3	Sequence 3, Appli
63	774	99.2	193	4	US-10-145-014-3	Sequence 3, Appli
64	774	99.2	233	2	US-08-971-317A-5	Sequence 5, Appli
65	774	99.2	233	3	US-09-193-663-5	Sequence 5, Appli
66	774	99.2	233	3	US-09-879-919-5	Sequence 5, Appli
67	774	99.2	233	3	US-09-782-980-43	Sequence 43, Appl
68	774	99.2	233	3	US-09-840-707A-14	Sequence 14, Appl
69	774	99.2	233	3	US-09-246-129B-3	Sequence 3, Appli
70	774	99.2	233	3	US-09-345-790-3	Sequence 3, Appli
71	774	99.2	233	3	US-09-929-493-3	Sequence 3, Appli
72	774	99.2	233	3	US-09-899-059-3	Sequence 3, Appli
73	774	99.2	233	3	US-09-131-237-3	Sequence 3, Appli
74	774	99.2	233	4	US-10-082-260-5	Sequence 5, Appli
75	774	99.2	233	4	US-10-012-452-10	Sequence 10, Appl
76	774	99.2	233	4	US-10-136-511-3	Sequence 3, Appli
77	774	99.2	233	4	US-10-145-014-22	Sequence 22, Appl
78	774	99.2	233	4	US-10-099-007A-2	Sequence 2, Appli
79	774	99.2	233	4	US-10-174-654-9	Sequence 9, Appli
80	774	99.2	233	4	US-10-151-882-42	Sequence 42, Appl
81	774	99.2	233	4	US-10-038-557A-14	Sequence 14, Appl
82	774	99.2	233	4	US-10-218-547-4	Sequence 4, Appli
83	774	99.2	233	4	US-10-226-294-4	Sequence 4, Appli
84	774	99.2	233	4	US-10-040-281A-20	Sequence 20, Appl
85	774	99.2	233	4	US-10-270-487-3	Sequence 3, Appli
86	774	99.2	233	4	US-10-247-671-182	Sequence 182, App
87	774	99.2	233	4	US-10-310-793-10	Sequence 10, Appl
88	774	99.2	233	4	US-10-279-687-5	Sequence 5, Appli
89	774	99.2	233	4	US-10-397-786A-2	Sequence 2, Appli
90	774	99.2	233	4	US-10-440-464-63	Sequence 63, Appl
91	774	99.2	233	4	US-10-202-062-4	Sequence 4, Appli
92	774	99.2	233	4	US-10-408-765A-1117	Sequence 1117, Ap
93	774	99.2	233	4	US-10-735-865-3	Sequence 3, Appli
94	774	99.2	233	4	US-10-739-042-3	Sequence 3, Appli
95	774	99.2	233	4	US-10-806-018-43	Sequence 43, Appl
96	774	99.2	233	4	US-10-799-345-18	Sequence 18, Appl
97	774	99.2	233	5	US-10-825-282-18	Sequence 18, Appl
98	774	99.2	233	5	US-10-688-845-75	Sequence 75, Appl
99	774	99.2	233	5	US-10-370-715B-20	Sequence 20, Appl
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ALIGNMENTS

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RESULT 1
US-10-668-178-15
; Sequence 15, Application US/10668178
; Publication No. US20050013795A1
; GENERAL INFORMATION:
;  APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
;  APPLICANT:  MAYUMI, Tadanori
;  APPLICANT:  TSUTSUMI, Yasuo
;  APPLICANT:  NAKAGAWA, Shinsaku
;  APPLICANT:  IKEGAMI, Hakuo
;  TITLE OF INVENTION: Biologically-active conjugate
;  FILE REFERENCE: MAYUMI2A
;  CURRENT APPLICATION NUMBER: US/10/668,178
;  CURRENT FILING DATE:  2003-09-24
;  PRIOR APPLICATION NUMBER: JP 83509/2002
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: JP 185387/2002
;  PRIOR FILING DATE: 2002-06-26
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 15
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Synthetic Construct
US-10-668-178-15

  Query Match            99.7%;  Score 778;  DB 5;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 3.2e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFSGQGCPSTHVLLTHTISRIAVSYQTRVNLLSAIASPCQRETPEGAEALPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 2
US-10-668-178-16
; Sequence 16, Application US/10668178
; Publication No. US20050013795A1
; GENERAL INFORMATION:
;  APPLICANT: KABUSHIKI KAISHA HAYASHIBARA SEIBUTSU KAGAKU KENKYUJO
;  APPLICANT:  MAYUMI, Tadanori
;  APPLICANT:  TSUTSUMI, Yasuo
;  APPLICANT:  NAKAGAWA, Shinsaku
;  APPLICANT:  IKEGAMI, Hakuo
;  TITLE OF INVENTION: Biologically-active conjugate
;  FILE REFERENCE: MAYUMI2A
;  CURRENT APPLICATION NUMBER: US/10/668,178
;  CURRENT FILING DATE:  2003-09-24
;  PRIOR APPLICATION NUMBER: JP 83509/2002
;  PRIOR FILING DATE: 2002-03-25
;  PRIOR APPLICATION NUMBER: JP 185387/2002
;  PRIOR FILING DATE: 2002-06-26
;  NUMBER OF SEQ ID NOS: 16
;  SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: synthetic (Variant protein of human tumor necrosis factor)
US-10-668-178-16

  Query Match            99.7%;  Score 778;  DB 5;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 3.2e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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RESULT 3
US-09-756-301A-1
; Sequence 1, Application US/09756301A
; Patent No. US20010027249A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-008
;  CURRENT APPLICATION NUMBER: US/09/756,301A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S.07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-756-301A-1

  Query Match            99.2%;  Score 774;  DB 3;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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US-09-927-703-1
; Sequence 1, Application US/09927703
; Patent No. US20020022720A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/09/927,703
;  CURRENT FILING DATE:  2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-927-703-1

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
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Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 5
US-09-854-280-19
; Sequence 19, Application US/09854280
; Patent No. US20020052027A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Li, Hanzhong
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES THEREOF
;  FILE REFERENCE: P1381R1C2
;  CURRENT APPLICATION NUMBER: US/09/854,280
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: US 09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/085,579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 60/113,621
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-854-280-19

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
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Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
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Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
                ||||||||  ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 6
US-09-934-465-13
; Sequence 13, Application US/09934465
; Patent No. US20020102233A1
; GENERAL INFORMATION:
;  APPLICANT: Ashkenazi, Avi J.
;  TITLE OF INVENTION: APO-2 LIGAND
;  FILE REFERENCE: 11669.22US03
;  CURRENT APPLICATION NUMBER: US/09/934,465
;  CURRENT FILING DATE:  2001-08-21
;  PRIOR APPLICATION NUMBER: 08/584,031
;  PRIOR FILING DATE: 1996-01-09
;  NUMBER OF SEQ ID NOS: 17
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-934-465-13

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
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Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 7
US-09-766-535A-1
; Sequence 1, Application US/09766535A
; Patent No. US20020106372A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-010
;  CURRENT APPLICATION NUMBER: US/09/766,535A
;  CURRENT FILING DATE:  2001-01-18
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-766-535A-1

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 8
US-09-854-208-19
; Sequence 19, Application US/09854208
; Patent No. US20020106743A1
; GENERAL INFORMATION:
;  APPLICANT: Chen, Jian
;  APPLICANT:  Filvaroff, Ellen
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Gurney, Austin
;  APPLICANT:  Li, Hanzhong
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: IL-17 HOMOLOGOUS POLYPEPTIDES AND THERAPEUTIC USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: P1381-R1
;  CURRENT APPLICATION NUMBER: US/09/854,208
;  CURRENT FILING DATE:  2001-05-10
;  PRIOR APPLICATION NUMBER: US/09/311,832
;  PRIOR FILING DATE: 1999-05-14
;  PRIOR APPLICATION NUMBER: US 60/085,579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: US 60/113,621
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 26
; SEQ ID NO 19
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-854-208-19

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 9
US-09-756-161A-1
; Sequence 1, Application US/09756161A
; Patent No. US20020132307A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-007
;  CURRENT APPLICATION NUMBER: US/09/756,161A
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
```

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;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S.07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-756-161A-1

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 10
US-09-903-327A-7
; Sequence 7, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
;  APPLICANT: Nemerow, Glen R.
;  APPLICANT:  Li, Erguang
;  TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
;  TITLE OF INVENTION:  GENE
;  TITLE OF INVENTION:  DELIVERY
;  FILE REFERENCE: 22908-1228
;  CURRENT APPLICATION NUMBER: US/09/903,327A
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 09/613,017
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 33
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Human
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (0)...(0)
;   OTHER INFORMATION: Tumor necrosis factor-alpha (TNF alpha, mature
;   OTHER INFORMATION: peptide)
US-09-903-327A-7

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 11
US-09-756-398B-1
; Sequence 1, Application US/09756398B
; Publication No. US20030017584A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-006
;  CURRENT APPLICATION NUMBER: US/09/756,398B
;  CURRENT FILING DATE:  2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S.07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-756-398B-1

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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RESULT 12
US-09-897-724-1
; Sequence 1, Application US/09897724
; Publication No. US20030175837A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-012
;  CURRENT APPLICATION NUMBER: US/09/897,724
;  CURRENT FILING DATE:  2001-07-02
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S.07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-897-724-1

  Query Match             99.2%;  Score 774;  DB 3;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 13
US-10-010-229-1
; Sequence 1, Application US/10010229
; Publication No. US20020114805A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/10/010,229
;  CURRENT FILING DATE:  2001-12-07
;  PRIOR APPLICATION NUMBER: US/09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-010-229-1

  Query Match             99.2%;  Score 774;  DB 4;  Length 157;
  Best Local Similarity   96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 14
US-10-043-450-1
; Sequence 1, Application US/10043450
; Publication No. US20020141996A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/10/043,450
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-043-450-1
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  Query Match           99.2%;  Score 774;  DB 4;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


RESULT 15
US-10-044-534-1
; Sequence 1, Application US/10044534
; Publication No. US20020146419A1
; GENERAL INFORMATION:
;  APPLICANT: Le, Junming
;  APPLICANT:  Vilcek, Jan
;  APPLICANT:  Daddona, Peter
;  APPLICANT:  Ghrayeb, John
;  APPLICANT:  Knight, David M.
;  APPLICANT:  Siegel, Scott
;  TITLE OF INVENTION: Anti-TNF Antibodies and Peptides of
;  TITLE OF INVENTION:  Human Tumor Necrosis Factor
;  FILE REFERENCE: 0975.1005-013
;  CURRENT APPLICATION NUMBER: US/10/044,534
;  CURRENT FILING DATE:  2002-01-10
;  PRIOR APPLICATION NUMBER: 09/927,703
;  PRIOR FILING DATE: 2001-08-10
;  PRIOR APPLICATION NUMBER: U.S. 09/756,398
;  PRIOR FILING DATE: 2001-01-08
;  PRIOR APPLICATION NUMBER: U.S. 09/133,119
;  PRIOR FILING DATE: 1998-08-12
;  PRIOR APPLICATION NUMBER: U.S. 08/570,674
;  PRIOR FILING DATE: 1995-12-11
;  PRIOR APPLICATION NUMBER: U.S. 08/324,799
;  PRIOR FILING DATE: 1994-10-18
;  PRIOR APPLICATION NUMBER: U.S. 08/192,102
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,861
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/192,093
;  PRIOR FILING DATE: 1994-02-04
;  PRIOR APPLICATION NUMBER: U.S. 08/010,406
;  PRIOR FILING DATE: 1993-01-29
;  PRIOR APPLICATION NUMBER: U.S. 08/013,413
;  PRIOR FILING DATE: 1993-02-02
;  PRIOR APPLICATION NUMBER: U.S. 07/943,852
;  PRIOR FILING DATE: 1992-09-11
;  PRIOR APPLICATION NUMBER: U.S. 07/853,606
;  PRIOR FILING DATE: 1992-03-18
;  PRIOR APPLICATION NUMBER: U.S. 07/670,827
;  PRIOR FILING DATE: 1991-03-18
;  NUMBER OF SEQ ID NOS: 19
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
;   LENGTH: 157
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-044-534-1

  Query Match           99.2%;  Score 774;  DB 4;  Length 157;
  Best Local Similarity  96.2%;  Pred. No. 9.6e-84;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db         61 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 120

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        121 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 157


Search completed: April  3, 2006, 08:23:15
Job time : 52 secs
```

GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:19:10 ; Search time 114 Seconds
(without alignments)
971.649 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 780
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	774	99.2	233	1	TNFA_HUMAN	P01375 homo sapien
2	774	99.2	233	2	Q5STB3_HUMAN	Q5stb3 homo sapien
3	767	98.3	233	1	TNFA_PAPSP	P33620 papio sp. (
4	765	98.1	232	1	TNFA_PANTR	Q8hzd9 pan troglod
5	756	96.9	233	1	TNFA_MACMU	P48094 macaca mula
6	753	96.5	233	1	TNFA_MACFA	P79337 macaca fasc
7	752	96.4	233	1	TNFA_PAPHU	O77510 papio hamad
8	749	96.0	233	1	TNFA_PAPAN	P59695 papio anubi
9	739	94.7	149	2	O97543_AOTNA	O97543 aotus nancy
10	733	94.0	233	1	TNFA_CANFA	P51742 canis famil
11	726	93.1	233	1	TNFA_FELCA	P19101 felis silve
12	702	90.0	233	1	TNFA_SAISC	Q8mkg8 saimiri sci
13	692	88.7	234	1	TNFA_HORSE	P29553 equus cabal
14	691	88.6	149	2	O97538_AOTVO	O97538 aotus vocif
15	691	88.6	149	2	Q9TTG8_AOTNI	Q9ttg8 aotus nigri
16	686	87.9	217	2	Q9BEG0_CYCDI	Q9beg0 cyclopes di
17	682	87.4	217	2	Q9BEG1_BRATR	Q9beg1 bradypus tr
18	675	86.5	233	1	TNFA_DELLE	Q8wnr1 delphinapte
19	673.5	86.3	232	1	TNFA_PIG	P23563 sus scrofa
20	657	84.2	233	1	TNFA_TURTR	Q9bea1 tursiops tr
21	647	82.9	217	2	Q9BEF4_CABUN	Q9bef4 cabassous u
22	638	81.8	138	2	Q9TTG7_AOTLE	Q9ttg7 aotus lemur
23	637	81.7	234	1	TNFA_CAPHI	P13296 capra hircu
24	634	81.3	234	2	Q53ZM5_CAPHI	Q53zm5 capra hircu
25	632.5	81.1	234	1	TNFA_CAVPO	P51435 cavia porce
26	631	80.9	216	2	Q9BEC4_TALEU	Q9bec4 talpa europ
27	629.5	80.7	235	1	TNFA_MOUSE	P06804 mus musculu
28	628	80.5	229	1	TNFA_CEREL	P51743 cervus elap
29	628	80.5	234	2	Q539C2_TUPTA	Q539c2 tupaia tana
30	627.5	80.4	235	1	TNFA_RABIT	P04924 oryctolagus
31	627	80.4	233	1	TNFA_BOVIN	Q06599 bos taurus
32	627	80.4	233	1	TNFA_BUBBU	P59693 bubalus bub
33	627	80.4	234	1	TNFA_BOSIN	P59684 bos indicus
34	625	80.1	234	1	TNFA_SHEEP	P23383 ovis aries
35	623.5	79.9	235	1	TNFA_PERLE	P36939 peromyscus
36	618.5	79.3	235	2	Q5W9H9_MERUN	Q5w9h9 meriones un
37	617.5	79.2	232	2	Q80XA4_PERMA	Q80xa4 peromyscus
38	614.5	78.8	235	1	TNFA_RAT	P16599 rattus norv
39	614.5	78.8	235	2	Q6EE11_RAT	Q6ee11 rattus norv
40	609	78.1	233	1	TNFA_CAMBA	Q75n23 camelus bac
41	609	78.1	233	1	TNFA_LAMGL	P59694 lama glama
42	606.5	77.8	156	2	Q91ZL4_SIGHI	Q91zl4 sigmodon hi
43	599.5	76.9	233	1	TNFA_MARMO	O35734 marmota mon
44	599.5	76.9	233	2	Q6X658_MARMO	Q6x658 marmota mon
45	598.5	76.7	216	2	Q9BEC9_OCHPR	Q9bec9 ochotona pr
46	595	76.3	215	2	Q9BEE8_ERIEU	Q9bee8 erinaceus e
47	584.5	74.9	216	2	O70332_MESAU	O70332 mesocricetu
48	580.5	74.4	217	2	Q9ERG6_PERMA	Q9erg6 peromyscus
49	579	74.2	217	2	Q9BEC5_TENEC	Q9bec5 tenrec ecau
50	573	73.5	233	1	TNFA_MACEU	O77764 macropus eu
51	572	73.3	215	2	Q99ND1_SCIVU	Q99nd1 sciurus vul
52	535	68.6	216	2	Q9BEE0_MACRU	Q9bee0 macropus ru
53	531	68.1	155	2	Q8HZD8_9PRIM	Q8hzd8 gorilla gor
54	530	67.9	155	2	Q8HZD7_PONPY	Q8hzd7 pongo pygma
55	501	64.2	155	2	Q8HZD5_SAGOE	Q8hzd5 saguinus oe
56	476	61.0	103	2	Q864Z0_PHYCA	Q864z0 physeter ca
57	469	60.1	103	2	Q864Y9_9EUTH	Q864y9 manis sp. c
58	454	58.2	99	2	Q864Y8_ELEMA	Q864y8 elephas max
59	449.5	57.6	102	2	Q80Z02_9HYST	Q80z02 trichys fas
60	448.5	57.5	214	2	Q9BEF3_DIDMA	Q9bef3 didelphis m
61	445	57.1	99	2	Q95LE8_CANFA	Q95le8 canis famil
62	442.5	56.7	102	2	Q80Z03_CASCN	Q80z03 castor cana
63	433.5	55.6	102	2	Q80Z04_9RODE	Q80z04 anomalurus
64	431.5	55.3	102	2	Q80Z06_DIPSA	Q80z06 dipus sagit
65	427	54.7	103	2	Q864Y7_TUPTA	Q864y7 tupaia tana
66	427	54.7	233	1	TNFA_TRIVU	P79374 trichosurus
67	394.5	50.6	102	2	Q80Z05_DIPME	Q80z05 dipodomys m
68	306	39.2	70	2	Q7YSE3_SHEEP	Q7yse3 ovis aries
69	287	36.8	101	2	Q9R136_MERUN	Q9r136 meriones un
70	281	36.0	65	2	Q95N81_CANFA	Q95n81 canis famil
71	271	34.7	70	2	Q75T06_RABIT	Q75t06 oryctolagus
72	257.5	33.0	205	1	TNFB_MARMO	Q9jm09 marmota mon
73	257	32.9	74	2	Q6PWY4_PIG	Q6pwy4 sus scrofa
74	254	32.6	253	2	Q7T194_ACASC	Q7t194 acanthopagr
75	252.5	32.4	197	1	TNFB_RABIT	P10154 oryctolagus
76	245.5	31.5	204	1	TNFB_BOVIN	Q06600 bos taurus
77	245.5	31.5	204	1	TNFB_CANFA	Q5wr07 canis famil
78	245	31.4	222	2	Q7T1U4_PAGMA	Q7t1u4 pagrus majo
79	241.5	31.0	204	1	TNFB_PIG	P26445 sus scrofa
80	241	30.9	253	1	TNFA_SPAAU	Q8jfg3 sparus aura
81	240	30.8	201	1	TNFB_MACEU	Q9xt48 macropus eu
82	239	30.6	241	2	Q6U817_LATJA	Q6u817 lateolabrax
83	237.5	30.4	202	2	Q80WE7_PERMA	Q80we7 peromyscus
84	235	30.1	202	1	TNFB_RAT	Q06332 rattus norv
85	233.5	29.9	202	1	TNFB_MOUSE	P09225 mus musculu
86	233.5	29.9	202	2	Q542S2_MOUSE	Q542s2 mus musculu
87	233.5	29.9	225	2	Q9IB42_PAROL	Q9ib42 paralichthy
88	233	29.9	250	2	Q4W8A0_FUGRU	Q4w8a0 fugu rubrip
89	231.5	29.7	225	2	Q9IB41_PAROL	Q9ib41 paralichthy
90	224.5	28.8	247	2	Q5VJN5_ORENI	Q5vjn5 oreochromis
91	217	27.8	246	2	Q9I976_ONCMY	Q9i976 oncorhynchu
92	215	27.6	246	2	Q9I970_ONCMY	Q9i970 oncorhynchu
93	212	27.2	188	2	Q5BMN1_SALSA	Q5bmn1 salmo salar
94	212	27.2	246	2	Q5BMN3_SALSA	Q5bmn3 salmo salar
95	210	26.9	127	2	Q9ERC9_MESAU	Q9erc9 mesocricetu
96	209.5	26.9	205	1	TNFB_HUMAN	P01374 homo sapien
97	209.5	26.9	205	1	TNFB_PANTR	P61125 pan troglod
98	209.5	26.9	205	2	Q5ST95_HUMAN	Q5st95 homo sapien
99	209.5	26.9	205	2	Q5STV3_HUMAN	Q5stv3 homo sapien
100	209.5	26.9	205	2	Q6FG55_HUMAN	Q6fg55 homo sapien

ALIGNMENTS

```
RESULT 1
TNFA_HUMAN
ID   TNFA_HUMAN     STANDARD;      PRT;   233 AA.
AC   P01375; O43647; Q9P1Q2; Q9UIV3;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=87217060; PubMed=3555974;
RA   Nedospasov S.A., Shakhov A.N., Turetskaya R.L., Mett V.A.,
RA   Azizov M.M., Georgiev G.P., Korobko V.G., Dobrynin V.N.,
RA   Filippov S.A., Bystrov N.S., Boldyreva E.F., Chuvpilo S.A.,
RA   Chumakov A.M., Shingarova L.N., Ovchinnikov Y.A.;
RT   "Tandem arrangement of genes coding for tumor necrosis factor (TNF-
RT   alpha) and lymphotoxin (TNF-beta) in the human genome.";
RL   Cold Spring Harb. Symp. Quant. Biol. 51:611-624(1986).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85086244; PubMed=6392892;
RA   Pennica D., Nedwin G.E., Hayflick J.S., Seeburg P.H., Derynck R.,
RA   Palladino M.A., Kohr W.J., Aggarwal B.B., Goeddel D.V.;
RT   "Human tumour necrosis factor: precursor structure, expression and
RT   homology to lymphotoxin.";
RL   Nature 312:724-729(1984).
RN   [3]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85137898; PubMed=3883195;
RA   Shirai T., Yamaguchi H., Ito H., Todd C.W., Wallace R.B.;
RT   "Cloning and expression in Escherichia coli of the gene for human
RT   tumour necrosis factor.";
RL   Nature 313:803-806(1985).
RN   [4]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86016093; PubMed=2995927;
RA   Nedwin G.E., Naylor S.L., Sakaguchi A.Y., Smith D.H.,
RA   Jarrett-Nedwin J., Pennica D., Goeddel D.V., Gray P.W.;
RT   "Human lymphotoxin and tumor necrosis factor genes: structure,
RT   homology and chromosomal localization.";
RL   Nucleic Acids Res. 13:6361-6373(1985).
RN   [5]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=85142190; PubMed=3856324;
RA   Wang A.M., Creasey A.A., Ladner M.B., Lin L.S., Strickler J.,
RA   van Arsdell J.N., Yamamoto R., Mark D.F.;
RT   "Molecular cloning of the complementary DNA for human tumor necrosis
RT   factor.";
RL   Science 228:149-154(1985).
RN   [6]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=86030296; PubMed=3932069;
RA   Marmenout A., Fransen L., Tavernier J., van der Heyden J., Tizard R.,
RA   Kawashima E., Shaw A., Johnson M.J., Semon D., Mueller R.,
RA   Ruysschaert M.R., van Vliet A., Fiers W.;
RT   "Molecular cloning and expression of human tumor necrosis factor and
RT   comparison with mouse tumor necrosis factor.";
RL   Eur. J. Biochem. 152:515-522(1985).
RN   [7]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=93272029; PubMed=8499947;
RA   Iris F.J.M., Bougueleret L., Prieur S., Caterina D., Primas G.,
RA   Perrot V., Jurka J., Rodriguez-Tome P., Claverie J.-M., Dausset J.,
RA   Cohen D.;
RT   "Dense Alu clustering and a potential new member of the NF kappa B
RT   family within a 90 kilobase HLA class III segment.";
RL   Nat. Genet. 3:137-145(1993).
RN   [8]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=99218514; PubMed=10202016;
RA   Neville M.J., Campbell R.D.;
RT   "A new member of the Ig superfamily and a V-ATPase G subunit are among
RT   the predicted products of novel genes close to the TNF locus in the
RT   human MHC.";
RL   J. Immunol. 162:4745-4754(1999).
RN   [9]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=14656967; DOI=10.1101/gr.1736803;
RA   Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,
RA   Campbell R.D., Hood L.;
RT   "Analysis of the gene-dense major histocompatibility complex class III
RT   region and its comparison to mouse.";
RL   Genome Res. 13:2621-2636(2003).
RN   [10]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Shiina S., Tamiya G., Oka A., Inoko H.;
RT   "Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
RN   [11]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA   Shiina T., Ota M., Katsuyama Y., Hashimoto N., Inoko H.;
RT   "Genome diversity in HLA: a new strategy for detection of genetic
RT   polymorphisms in expressed genes within the HLA class III and class I
RT   regions.";
RL   Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
RN   [12]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Rieder M.J., Carrington D.P., Chung M.-W., Lee K.L., Poel C.L., Yi Q.,
RA   Nickerson D.A.;
RT   "SeattleSNPs. NHLBI HL66682 program for genomic applications, UW-
RT   FHCRC, Seattle, WA (URL: http://pga.gs.washington.edu).";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
RN   [13]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA], AND VARIANT LEU-84.
RA   Rieder M.J., Livingston R.J., Daniels M.R., Montoya M.A., Chung M.-W.,
RA   Miyamoto K.E., Nguyen C.P., Nguyen D.A., Poel C.L., Robertson P.D.,
RA   Schackwitz W.S., Sherwood J.K., Witrak L.A., Nickerson D.A.;
RT   "NIEHS-SNPs, environmental genome project, NIEHS ES15478, Department
RT   of Genome Sciences, Seattle, WA (URL: http://egp.gs.washington.edu).";
RL   Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.
RN   [14]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC   TISSUE=Blood;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [15]
RP   NUCLEOTIDE SEQUENCE OF 77-233.
RA   Jang J.S., Kim B.E.;
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RL   Submitted (JAN-1998) to the EMBL/GenBank/DDBJ databases.
RN   [16]
RP   NUCLEOTIDE SEQUENCE OF 84-214.
RC   TISSUE=Prostatic carcinoma;
RA   Shao C., Yan W., Zhu F., Yue W., Chai Y., Zhao Z., Wang C.;
RL   Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
RN   [17]
RP   PHOSPHORYLATION (MEMBRANE FORM).
RX   MEDLINE=96170872; PubMed=8597870;
RA   Pocsik E., Duda E., Wallach D.;
RT   "Phosphorylation of the 26 kDa TNF precursor in monocytic cells and in
RT   transfected HeLa cells.";
RL   J. Inflamm. 45:152-160(1995).
RN   [18]
RP   PHOSPHORYLATION BY CK1, AND DEPHOSPHORYLATION.
RX   MEDLINE=99221647; PubMed=10205166; DOI=10.1093/emboj/18.8.2119;
RA   Watts A.D., Hunt N.H., Wanigasekara Y., Bloomfield G., Wallach D.,
RA   Roufogalis B.D., Chaudhri G.;
RT   "A casein kinase I motif present in the cytoplasmic domain of members
RT   of the tumour necrosis factor ligand family is implicated in 'reverse
RT   signalling'.";
RL   EMBO J. 18:2119-2126(1999).
RN   [19]
RP   MUTAGENESIS.
RX   MEDLINE=91184128; PubMed=2009860;
RA   Ostade X.V., Tavernier J., Prange T., Fiers W.;
RT   "Localization of the active site of human tumour necrosis factor
RT   (hTNF) by mutational analysis.";
RL   EMBO J. 10:827-836(1991).
RN   [20]
RP   MYRISTOYLATION.
RX   MEDLINE=93018820; PubMed=1402651; DOI=10.1084/jem.176.4.1053;
RA   Stevenson F.T., Bursten S.L., Locksley R.M., Lovett D.H.;
RT   "Myristyl acylation of the tumor necrosis factor alpha precursor on
RT   specific lysine residues.";
RL   J. Exp. Med. 176:1053-1062(1992).
RN   [21]
RP   CLEAVAGE BY ADAM17.
RX   MEDLINE=97186575; PubMed=9034191;
RA   Moss M.L., Jin S.-L.C., Milla M.E., Burkhart W., Carter H.L.,
RA   Chen W.-J., Clay W.C., Didsbury J.R., Hassler D., Hoffman C.R.,
RA   Kost T.A., Lambert M.H., Leesnitzer M.A., McCauley P., McGeehan G.,
RA   Mitchell J., Moyer M., Pahel G., Rocque W., Overton L.K., Schoenen F.,
RA   Seaton T., Su J.-L., Warner J., Willard D., Becherer J.D.;
RT   "Cloning of a disintegrin metalloproteinase that processes precursor
RT   tumour-necrosis factor-alpha.";
RL   Nature 385:733-736(1997).
RN   [22]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=89159409; PubMed=2922050; DOI=10.1038/338225a0;
RA   Jones E.Y., Stuart D.I., Walker N.P.;
RT   "Structure of tumour necrosis factor.";
RL   Nature 338:225-228(1989).
RN   [23]
RP   X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX   MEDLINE=91193276; PubMed=1964681;
RA   Jones E.Y., Stuart D.I., Walker N.P.;

  Query Match             99.2%;  Score 774;  DB 1;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 7.6e-77;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233
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RESULT 2
Q5STB3_HUMAN
ID   Q5STB3_HUMAN PRELIMINARY;      PRT;   233 AA.
AC   Q5STB3;
DT   01-FEB-2005 (TrEMBLrel. 29, Created)
DT   01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT   13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE   Tumor necrosis factor (TNF superfamily, member 2).
GN   Name=TNF;
GN   ORFNames=DAQB-87N14.5-001, DASS-280D8.2-001, XXbac-BCX270M2.1-001,
GN   XXbac-BPG296P20.12-001;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Tracey A.;
RL   Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL662847; CAI17678.1; -; Genomic_DNA.
DR   EMBL; AL929587; CAI18649.1; -; Genomic_DNA.
DR   EMBL; AL662801; CAI18292.1; -; Genomic_DNA.
DR   EMBL; BX248519; CAI41940.1; -; Genomic_DNA.
DR   SMR; Q5STB3; 82-233.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
SQ   SEQUENCE   233 AA;  25644 MW;  3DF90F96C9031FFE CRC64;

  Query Match             99.2%;  Score 774;  DB 2;  Length 233;
  Best Local Similarity   96.2%;  Pred. No. 7.6e-77;
  Matches  151;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| ||||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233
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RESULT 3
TNFA_PAPSP
ID   TNFA_PAPSP     STANDARD;      PRT;   233 AA.
AC   P33620;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio sp. (Baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
```

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OX   NCBI_TaxID=61183;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RA   Sanjanwala M., Edwards A.;
RL   Submitted (SEP-1991) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X62141; CAA44068.1; -; Genomic_DNA.
DR   PIR; S22052; S22052.
DR   HSSP; P01375; 1A8M.
DR   SMR; P33620; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25557 MW;  455360B48DC74173 CRC64;

  Query Match             98.3%;  Score 767;  DB 1;  Length 233;
  Best Local Similarity   95.5%;  Pred. No. 4.5e-76;
  Matches  150;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||| ||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233
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RESULT 4
TNFA_PANTR
ID   TNFA_PANTR     STANDARD;      PRT;   232 AA.
AC   Q8HZD9;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC   Pan.
OX   NCBI_TaxID=9598;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22381002; PubMed=12493009;
RX   DOI=10.1034/j.1600-065X.2002.19008.x;
RA   Kulski J.K., Shiina T., Anzai T., Kohara S., Inoko H.;
RT   "Comparative genomic analysis of the MHC: the evolution of class I
RT   duplication blocks, diversity and complexity from shark to man.";
RL   Immunol. Rev. 190:95-122(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   MEDLINE=22709134; PubMed=12799463; DOI=10.1073/pnas.1230533100;
RA   Anzai T., Shiina T., Kimura N., Yanagiya K., Kohara S., Shigenari A.,
RA   Yamagata T., Kulski J.K., Naruse T.K., Fujimori Y., Fukuzumi Y.,
RA   Yamazaki M., Tashiro H., Iwamoto C., Umehara Y., Imanishi T.,
RA   Meyer A., Ikeo K., Gojobori T., Bahram S., Inoko H.;
RT   "Comparative sequencing of human and chimpanzee MHC class I regions
RT   unveils insertions/deletions as the major path to genomic
RT   divergence.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:7708-7713(2003).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 33-186.
RA   O'Huigin C., Tichy H., Klein J.;
RT   "Molecular evolution in higher primates; gene specific and organism
RT   specific characteristics.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB054536; BAB83882.1; -; Genomic_DNA.
DR   EMBL; BA000041; BAC78157.1; -; Genomic_DNA.
DR   EMBL; AY091964; AAM76582.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8HZD9; 81-232.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
```

```
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN          1    232       Tumor necrosis factor, membrane form (By
FT                                 similarity).
FT   CHAIN         77    232       Tumor necrosis factor, soluble form (By
FT                                 similarity).
FT   TOPO_DOM       1     34       Cytoplasmic (Potential).
FT   TRANSMEM      35     57       Signal-anchor for type II membrane
FT                                 protein (By similarity).
FT   TOPO_DOM      58    232       Extracellular (Potential).
FT   SITE          76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES        2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID     144    176       By similarity.
FT   CONFLICT      77     77       G -> VR (in Ref. 3).
SQ   SEQUENCE   232 AA;  25446 MW;  E4D71B19C6AE0D03 CRC64;

  Query Match             98.1%;  Score 765;  DB 1;  Length 232;
  Best Local Similarity   96.1%;  Pred. No. 7.4e-76;
  Matches  149;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 SSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 62
              |||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 SSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQV 137

Qy         63 LFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGG 122
              || |||||||||||||||||||||||| ||||||| ||||||||||||| ||||||||||
Db        138 LFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGG 197

Qy        123 VFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||| ||||||||||||||||||||||||||||||
Db        198 VFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 232


RESULT 5
TNFA_MACMU
ID   TNFA_MACMU     STANDARD;      PRT;   233 AA.
AC   P48094; Q5TM21; Q8HZD6;
DT   01-FEB-1996 (Rel. 33, Created)
DT   01-FEB-1996 (Rel. 33, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=96003435; PubMed=7561102;
RA   Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RT   "Comparative sequence analysis of cytokine genes from human and
RT   nonhuman primates.";
RL   J. Immunol. 155:3946-3954(1995).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX   PubMed=15269276; DOI=10.1093/molbev/msh216;
RA   Kulski J.K., Anzai T., Shiina T., Inoko H.;
RT   "Rhesus macaque class I duplicon structures, organization, and
RT   evolution within the alpha block of the major histocompatibility
RT   complex.";
RL   Mol. Biol. Evol. 21:2079-2091(2004).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA] OF 33-187.
RA   O'Huigin C., Tichy H., Klein J.;
RT   "Molecular evolution in higher primates; gene specific and organism
RT   specific characteristics.";
RL   Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; U19850; AAA86712.1; -; mRNA.
DR   EMBL; AB128049; BAD69724.1; -; Genomic_DNA.
DR   EMBL; AY091967; AAM76585.1; -; Genomic_DNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P48094; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN          1    233       Tumor necrosis factor, membrane form.
FT   CHAIN         77    233       Tumor necrosis factor, soluble form.
FT   TOPO_DOM       1     35       Cytoplasmic (Potential).
FT   TRANSMEM      36     56       Signal-anchor for type II membrane
FT                                 protein (Potential).
FT   TOPO_DOM      57    233       Extracellular (Potential).
FT   SITE          76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES        2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID     145    177       By similarity.
SQ   SEQUENCE   233 AA;  25630 MW;  9F6F85050595FD59 CRC64;

  Query Match             96.9%;  Score 756;  DB 1;  Length 233;
  Best Local Similarity   94.3%;  Pred. No. 7.4e-75;
  Matches  148;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||| |||||||||||||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233
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RESULT 6
TNFA_MACFA
ID   TNFA_MACFA     STANDARD;      PRT;   233 AA.
AC   P79337;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Macaca.
OX   NCBI_TaxID=9541;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Lymphocyte;
RA   Tatsumi M.;
RT   "Molecular cloning and expression of cynomolgus monkey TNF-alpha.";
RL   Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AB000513; BAA19131.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P79337; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25558 MW;  6ABF2C3AB132C217 CRC64;

  Query Match             96.5%;  Score 753;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 1.6e-74;
  Matches  147;  Conservative    1;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||:|||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALVANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||| |||||||||||||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 7
TNFA_PAPHU
ID   TNFA_PAPHU     STANDARD;      PRT;   233 AA.
AC   O77510;
DT   15-DEC-1998 (Rel. 37, Created)
DT   15-DEC-1998 (Rel. 37, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio hamadryas ursinus (Chacma baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=36229;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RX   MEDLINE=98147379; PubMed=9488055; DOI=10.1016/S0161-5890(97)00124-7;
RA   Haudek S.B., Redl H., Schlag G., Giroir B.P.;
RT   "Complementary DNA (cDNA) sequence of baboon tumor necrosis factor
RT   alpha.";
RL   Mol. Immunol. 34:1041-1042(1997).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF019963; AAC31675.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O77510; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
```

```
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25658 MW;  B9403255058D4A03 CRC64;

  Query Match             96.4%;  Score 752;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 2e-74;
  Matches  147;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| || ||||||||||||||||||||||||||||| ||||||||||||||||
Db         77 VRSSSRTPSDKPVVHVVANPQAEGQLQWLNRRANALLANGVELTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||| |||||||||||||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 8
TNFA_PAPAN
ID   TNFA_PAPAN     STANDARD;      PRT;   233 AA.
AC   P59695;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Papio anubis (Olive baboon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC   Cercopithecidae; Cercopithecinae; Papio.
OX   NCBI_TaxID=9555;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21383618; PubMed=11491535; DOI=10.1007/s002510100322;
RA   Villinger F.J., Bostik P., Mayne A.E., King C.L., Genain C.P.,
RA   Weiss W.R., Ansari A.A.;
RT   "Cloning, sequencing, and homology analysis of nonhuman primate
RT   Fas/Fas-ligand and co-stimulatory molecules.";
RL   Immunogenetics 53:315-328(2001).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AY234222; AAO85335.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P59695; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                similarity).
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                similarity).
FT   TOPO_DOM      1     34       Cytoplasmic (Potential).
FT   TRANSMEM     35     57       Signal-anchor for type II membrane
FT                                protein (By similarity).
FT   TOPO_DOM     58    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25736 MW;  0C477F9EB6CC9909 CRC64;

  Query Match             96.0%;  Score 749;  DB 1;  Length 233;
  Best Local Similarity   93.6%;  Pred. No. 4.4e-74;
  Matches  147;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||  ||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVEPTDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||| |||||||||||||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFKGQGCPSNHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233


RESULT 9
O97543_AOTNA
ID   O97543_AOTNA PRELIMINARY;      PRT;   149 AA.
AC   O97543;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus nancymaae (Ma's night monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=37293;
RN   [1]
```

```
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
DR   EMBL; AF014513; AAD01539.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O97543; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
FT   NON_TER     149     149
SQ   SEQUENCE   149 AA;  16466 MW;  3C2A6140778EFA8A CRC64;

  Query Match             94.7%;  Score 739;  DB 2;  Length 149;
  Best Local Similarity   96.0%;  Pred. No. 3.2e-73;
  Matches  143;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFKGQ 60

Qy         68 GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
              |||||||||||||||||||| ||||||| |||||||||||| ||||||||||||||
Db         61 GCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYLGGVFQLE 120

Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIA 156
              ||||||||||||||||||||||||||||
Db        121 KGDRLSAEINRPDYLDFAESGQVYFGIIA 149


RESULT 10
TNFA_CANFA
ID   TNFA_CANFA     STANDARD;      PRT;   233 AA.
AC   P51742; Q28339;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC   Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Fiers W.;
RT   "Tumour necrosis factor.";
RL   (In) Sim E. (eds.);
RL   The natural immune system humoral factors, pp.65-119, IRL Press,
RL   Oxford (1993).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RA   Zucker K., Lu P., Fuller L., Asthana D., Esquenazi V., Miller J.;
RT   "Cloning and expression of the cDNA for canine tumor necrosis factor-
RT   alpha in E. coli.";
RL   Lymphokine Res. 13:191-196(1994).
RN   [3]
RP   NUCLEOTIDE SEQUENCE [GENOMIC DNA].
RA   Wagner J.L., Palti Y., DiDario D.D.;
RT   "Genomic map of a portion of the canine MHC class I histocompatibility
RT   complex.";
RL   Submitted (SEP-2003) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   NUCLEOTIDE SEQUENCE [MRNA] OF 74-205.
RC   STRAIN=Beagle; TISSUE=Blood;
RA   Gilmore W.H., Carter S.D., Bennett M., Barnes A., Kelly D.F.;
RT   "Expression of canine TNF, IL-1 and IL-6 mRNAs in peripheral blood
RT   monocytes and cell lines.";
RL   Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X94932; CAA64403.1; -; Genomic_DNA.
DR   EMBL; S74068; AAB32391.1; -; mRNA.
DR   EMBL; AY423389; AAR27885.1; -; Genomic_DNA.
DR   EMBL; Z70046; CAA93908.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; P51742; 82-233.
DR   Ensembl; ENSCAFG00000000517; Canis familiaris.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
FT   CONFLICT     59     60       QR -> PE (in Ref. 2).
FT   CONFLICT     66     66       G -> C (in Ref. 2).
FT   CONFLICT     74     74       A -> V (in Ref. 4).
FT   CONFLICT    111    111       A -> D (in Ref. 2).
FT   CONFLICT    116    116       G -> D (in Ref. 2).
FT   CONFLICT    134    135       IY -> DS (in Ref. 2).
```

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SQ   SEQUENCE   233 AA;  25447 MW;  7B2588FBC8B25340 CRC64;

  Query Match             94.0%;  Score 733;  DB 1;  Length 233;
  Best Local Similarity   89.8%;  Pred. No. 2.6e-72;
  Matches  141;  Conservative    6;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |:|||||||| |||||||||:||||||||:|||||||||||||| ||||:|||:|||||||
Db         77 VKSSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLIVPSDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||| |||||| ||||||| |||||||||| || ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQRETPEGTEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |:||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPNYLDFAESGQVYFGIIAL 233


RESULT 11
TNFA_FELCA
ID   TNFA_FELCA     STANDARD;      PRT;   233 AA.
AC   P19101; Q8HYM0;
DT   01-NOV-1990 (Rel. 16, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Felis silvestris catus (Cat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Felidae;
OC   Felinae; Felis.
OX   NCBI_TaxID=9685;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Blood;
RX   MEDLINE=91016860; PubMed=2216740;
RA   McGraw R.A., Coffee B.W., Otto C.M., Drews R.T., Rawlings C.A.;
RT   "Gene sequence of feline tumor necrosis factor alpha.";
RL   Nucleic Acids Res. 18:5563-5563(1990).
RN   [2]
RP   NUCLEOTIDE SEQUENCE [MRNA].
RC   TISSUE=Bone marrow;
RA   Daniel S.L., Brenner C.A., Legendre A.M., Soloman A., Rouse B.T.;
RT   "Feline cytokines TNF alpha and IL-1 beta: PCR cloning and sequencing
RT   of cDNA.";
RL   Anim. Biotechnol. 3:117-121(1992).
RN   [3]
RP   NUCLEOTIDE SEQUENCE OF 95-185.
RA   Susott E.E., Rollo W.A., Venta P.J., Ewart S.L.;
RT   "Characterization of 8 feline type I markers.";
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; X54000; CAA37948.1; -; Genomic_DNA.
DR   EMBL; M92061; AAA30818.1; -; mRNA.
DR   EMBL; AF459810; AAO15590.1; -; Genomic_DNA.
DR   PIR; S11688; S11688.
DR   HSSP; P01375; 4TSV.
DR   SMR; P19101; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form.
FT   CHAIN        77    233       Tumor necrosis factor, soluble form.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
FT   CONFLICT     28     28       G -> R (in Ref. 2).
FT   CONFLICT    104    104       W -> R (in Ref. 1).
FT   CONFLICT    141    141       T -> K (in Ref. 3).
FT   CONFLICT    151    151       L -> H (in Ref. 2).
FT   CONFLICT    155    155       T -> A (in Ref. 1).
FT   CONFLICT    210    210       T -> A (in Ref. 2).
SQ   SEQUENCE   233 AA;  25382 MW;  03E51823A7863510 CRC64;

  Query Match             93.1%;  Score 726;  DB 1;  Length 233;
  Best Local Similarity   89.8%;  Pred. No. 1.5e-71;
  Matches  141;  Conservative    4;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||| |||||||||:||||||||:|||||||||||||| |||| |||:|||||||
Db         77 LRSSSRTPSDKPVAHVVANPEAEGQLQWLSRRANALLANGVELTDNQLKVPSDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||| |||||| |||||||| |||||||||||||| ||||||||
Db        137 QVLFTGQGCPSTHVLLTHTISRFAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||| ||| | |||||||||||||||||
Db        197 GGVFQLEKGDRLSTEINLPAYLDFAESGQVYFGIIAL 233


RESULT 12
TNFA_SAISC
ID   TNFA_SAISC     STANDARD;      PRT;   233 AA.
AC   Q8MKG8;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Saimiri sciureus (Common squirrel monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Cebinae; Saimiri.
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OX   NCBI_TaxID=9521;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=21972723; PubMed=11976788; DOI=10.1007/s00251-002-0443-y;
RA   Heraud J.M., Lavergne A., Kazanji M.;
RT   "Molecular cloning, characterization, and quantification of squirrel
RT   monkey (Saimiri sciureus) Th1 and Th2 cytokines.";
RL   Immunogenetics 54:20-29(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22516846; PubMed=12628762; DOI=10.1016/S0165-2427(03)00018-7;
RA   Merien F., Lavergne A., Behr C., Contamin H.;
RT   "Sequencing and analysis of genomic DNA and cDNA encoding TNF-alpha in
RT   the squirrel monkey (Saimiri sciureus).";
RL   Vet. Immunol. Immunopathol. 92:37-43(2003).
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation (By similarity).
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; AF294760; AAK92047.1; -; mRNA.
DR   EMBL; AJ437697; CAD27179.1; -; Genomic_DNA.
DR   EMBL; AJ437698; CAD27180.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q8MKG8; 82-233.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    233       Tumor necrosis factor, membrane form (By
FT                                 similarity).
FT   CHAIN        77    233       Tumor necrosis factor, soluble form (By
FT                                 similarity).
FT   TOPO_DOM      1     32       Cytoplasmic (Potential).
FT   TRANSMEM     33     55       Signal-anchor for type II membrane
FT                                 protein (By similarity).
FT   TOPO_DOM     56    233       Extracellular (Potential).
FT   SITE         76     77       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    145    177       By similarity.
SQ   SEQUENCE   233 AA;  25578 MW;  197FB066F744FCAD CRC64;

  Query Match             90.0%;  Score 702;  DB 1;  Length 233;
  Best Local Similarity   87.3%;  Pred. No. 6.8e-69;
  Matches  137;  Conservative    5;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||| ||| ||||||||||||||||||||||||||||||||||||||:||||:||
Db         77 VRSSSRIPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSDGLYLVYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||  ||||:||||||||  |||||||  |||||||| ||:  ||||||||
Db        137 QVLFKGQGCPSTFTLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTHPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||: || || ||||||||||||
Db        197 GGVFQLEKGDRLSAEISPPDSLDLAESGQVYFGIIAL 233


RESULT 13
TNFA_HORSE
ID   TNFA_HORSE     STANDARD;      PRT;   234 AA.
AC   P29553; Q9TTJ3;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   13-SEP-2005 (Rel. 48, Last annotation update)
DE   Tumor necrosis factor precursor (TNF-alpha) (Tumor necrosis factor
DE   ligand superfamily member 2) (TNF-a) (Cachectin) [Contains: Tumor
DE   necrosis factor, membrane form; Tumor necrosis factor, soluble form].
GN   Name=TNF; Synonyms=TNFA, TNFSF2;
OS   Equus caballus (Horse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
OX   NCBI_TaxID=9796;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=92084125; PubMed=1748301; DOI=10.1016/0378-1119(91)90333-7;
RA   Su X., Morris D.D., McGraw R.A.;
RT   "Cloning and characterization of gene TNF alpha encoding equine tumor
RT   necrosis factor alpha.";
RL   Gene 107:319-321(1991).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   STRAIN=Thoroughbred; TISSUE=Artery;
RA   Ishida N., Sato F., Hasegawa T.;
RT   "Molecular cloning of equine tumor necrosis factor-alpha mRNA.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Cytokine that binds to TNFRSF1A/TNFR1 and
CC       TNFRSF1B/TNFBR. It is mainly secreted by macrophages and can
CC       induce cell death of certain tumor cell lines. It is potent
CC       pyrogen causing fever by direct action or by stimulation of
CC       interleukin 1 secretion and is implicated in the induction of
CC       cachexia, Under certain conditions it can stimulate cell
CC       proliferation and induce cell differentiation.
CC   -!- SUBUNIT: Homotrimer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Type II membrane protein. Also exists as an
CC       extracellular soluble form (By similarity).
CC   -!- PTM: The soluble form derives from the membrane form by
CC       proteolytic processing (By similarity).
CC   -!- PTM: The membrane form, but not the soluble form, is
CC       phosphorylated on serine residues. Dephosphorylation of the
CC       membrane form occurs by binding to soluble TNFRSF1A/TNFR1 (By
CC       similarity).
CC   -!- SIMILARITY: Belongs to the tumor necrosis factor family.
CC   ---------------------------------------------------------------------
CC   This Swiss-Prot entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   ---------------------------------------------------------------------
DR   EMBL; M64087; AAA30959.1; -; Genomic_DNA.
DR   EMBL; AB035735; BAA88349.1; -; mRNA.
DR   PIR; JQ1344; JQ1344.
DR   HSSP; P01375; 1A8M.
DR   SMR; P29553; 83-234.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
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DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   PANTHER; PTHR11471:SF4; TNF_alpha; 1.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
KW   Cytokine; Phosphorylation; Signal-anchor; Transmembrane.
FT   CHAIN         1    234       Tumor necrosis factor, membrane form.
FT   CHAIN        78    234       Tumor necrosis factor, soluble form.
FT   TOPO_DOM      1     35       Cytoplasmic (Potential).
FT   TRANSMEM     36     56       Signal-anchor for type II membrane
FT                                protein (Potential).
FT   TOPO_DOM     57    234       Extracellular (Potential).
FT   SITE         77     78       Cleavage (by ADAM17) (By similarity).
FT   MOD_RES       2      2       Phosphoserine (by CK1) (By similarity).
FT   DISULFID    146    178       By similarity.
FT   CONFLICT    177    179       PCH -> LAN (in Ref. 2).
SQ   SEQUENCE   234 AA;  25469 MW;  E79ACE91143DF373 CRC64;

  Query Match             88.7%;  Score 692;  DB 1;  Length 234;
  Best Local Similarity   85.4%;  Pred. No. 8.6e-68;
  Matches  134;  Conservative   10;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||| ||||||||||||||||||: ||||||||||:| ||||||| :|||||||
Db         78 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSGRANALLANGVKLTDNQLVVPLDGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| ||||||||||||||||:|||| : ||||||| |||  |:|| ||| |||||||||
Db        138 QVLFKGQGCPSTHVLLTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPWYEPIYL 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||:|||||||:|:||||||||||||||||
Db        198 GGVFQLEKGDQLSAEINQPNYLDFAESGQVYFGIIAL 234


RESULT 14
O97538_AOTVO
ID   O97538_AOTVO PRELIMINARY;      PRT;   149 AA.
AC   O97538;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus vociferans (Spix's owl monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=57176;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
DR   EMBL; AF014508; AAD01534.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; O97538; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   SMART; SM00207; TNF; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
FT   NON_TER     149     149
SQ   SEQUENCE   149 AA;  16415 MW;  86F1B9BCED16E689 CRC64;

  Query Match             88.6%;  Score 691;  DB 2;  Length 149;
  Best Local Similarity   89.3%;  Pred. No. 6.5e-68;
  Matches  133;  Conservative    4;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              ||| ||||||||||||||||||||||||||||||||||||||||||:|||||| ||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLVYSQVLFKGQ 60

Qy         68 GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
              ||||| :|||:|||||||||  ||||||| |||||||| ||:  |||||||||||||||
Db         61 GCPSTFMLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTNPWYEPIYLGGVFQLE 120

Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIA 156
              ||||||||| ||||| ||||||||||||
Db        121 KGDRLSAEINLPDYLDLAESGQVYFGIIA 149


RESULT 15
Q9TTG8_AOTNI
ID   Q9TTG8_AOTNI PRELIMINARY;      PRT;   149 AA.
AC   Q9TTG8;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Tumor necrosis factor alpha (Fragment).
GN   Name=TNF-alpha;
OS   Aotus nigriceps (Black-headed owl monkey).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC   Aotinae; Aotus.
OX   NCBI_TaxID=57175;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RX   MEDLINE=22354194; PubMed=12466897; DOI=10.1007/s00251-002-0512-2;
RA   Hernandez E.C., Suarez C.F., Mendez J.A., Echeverry S.J.,
RA   Murillo L.A., Patarroyo M.E.;
RT   "Identification, cloning, and sequencing of different cytokine genes
RT   in four species of owl monkey.";
RL   Immunogenetics 54:645-653(2002).
DR   EMBL; AF097328; AAF21303.1; -; mRNA.
DR   HSSP; P01375; 4TSV.
DR   SMR; Q9TTG8; 1-149.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005164; F:tumor necrosis factor receptor binding; IEA.
DR   GO; GO:0006955; P:immune response; IEA.
DR   InterPro; IPR006053; TNF_abc.
DR   InterPro; IPR002959; TNF_alpha.
DR   InterPro; IPR006052; TNF_family.
DR   InterPro; IPR003636; TNF_subf.
DR   Pfam; PF00229; TNF; 1.
DR   PRINTS; PR01234; TNECROSISFCT.
DR   PRINTS; PR01235; TNFALPHA.
DR   ProDom; PD002012; TNF_subf; 1.
DR   PROSITE; PS00251; TNF_1; 1.
DR   PROSITE; PS50049; TNF_2; 1.
FT   NON_TER       1       1
FT   NON_TER     149     149
SQ   SEQUENCE   149 AA;  16415 MW;  86F1B9BCED16E689 CRC64;

  Query Match             88.6%;  Score 691;  DB 2;  Length 149;
  Best Local Similarity   89.3%;  Pred. No. 6.5e-68;
  Matches  133;  Conservative    4;  Mismatches   12;  Indels    0;  Gaps    0;
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Qy          8 PSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQ 67
              ||| |||||||||||||||||||||||||||||||||||||||||||||||:|||||| ||
Db          1 PSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLVYSQVLFKGQ 60

Qy         68 GCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
              ||||| :||||:||||||||| |||||| |||||||| ||:  ||||||||||||||
Db         61 GCPSTFMLLTHSISRIAVSYQAKVNLLSAIKSPCQRETPRGAKTNPWYEPIYLGGVFQLE 120

Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIA 156
              ||||||||| ||||| ||||||||||||
Db        121 KGDRLSAEINLPDYLDLAESGQVYFGIIA 149


Search completed: April 3, 2006, 08:21:14
Job time : 116 secs
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GenCore version 5.1.7

OM protein - protein search, using sw model

Run on: April 3, 2006, 08:19:11 ; Search time 16 Seconds
(without alignments)
944.127 Million cell updates/sec

Title: US-10-668-178-2
Perfect score: 780
Sequence: 1 VRSSSRTPSDXPVAHVVANP.....RPDYLDFAESGQVYFGIIAL 157

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	774	99.2	233	1	QWHUN	tumor necrosis fac
2	767	98.3	233	1	S22052	tumor necrosis fac
3	707	90.6	233	2	S11688	tumor necrosis fac
4	692	88.7	234	1	JQ1344	tumor necrosis fac
5	673.5	86.3	232	1	S12606	tumor necrosis fac
6	629.5	80.7	235	1	QWMSN	tumor necrosis fac
7	627.5	80.4	234	1	A25451	tumor necrosis fac
8	627	80.4	185	2	S52715	tumor necrosis fac
9	627	80.4	233	1	S24642	tumor necrosis fac
10	625	80.1	234	1	JH0529	tumor necrosis fac
11	623.5	79.9	235	2	I54490	tumor necrosis fac
12	620.5	79.6	193	2	S06192	tumor necrosis fac
13	614.5	78.8	235	2	JU0029	tumor necrosis fac
14	252.5	32.4	197	1	JH0309	tumor necrosis fac
15	245.5	31.5	204	1	S24641	lymphotoxin - bovi
16	241.5	31.0	204	1	S17289	tumor necrosis fac
17	235	30.1	202	1	JN0869	tumor necrosis fac
18	233.5	29.9	202	1	B27303	tumor necrosis fac
19	209.5	26.9	205	1	QWHUX	lymphotoxin alpha
20	166.5	21.3	278	2	A49266	fas ligand - rat
21	165	21.2	244	2	A46066	lymphotoxin beta -
22	160.5	20.6	279	2	A53062	Fas ligand - mouse
23	151	19.4	281	2	I38707	Fas ligand - human
24	139	17.8	306	2	I49139	lymphotoxin-beta -
25	127	16.3	260	2	S21738	CD40 ligand - mous
26	113	14.5	261	2	I53476	CD40 ligand - huma
27	112	14.4	261	2	S53090	CD40 ligand - bovi
28	73	9.4	286	2	S56436	hypothetical 29.7K
29	72.5	9.3	887	2	AD2009	hypothetical prote
30	72	9.2	724	2	A53371	glutamate-ammonia
31	71.5	9.2	799	2	C82929	ATP synthase alpha
32	71	9.1	265	2	B84108	hypothetical prote
33	71	9.1	286	2	E91277	probable oxidoredu
34	71	9.1	286	2	E86118	probable oxidoredu
35	70.5	9.0	264	2	AE2100	phosphonate ABC tr
36	70.5	9.0	403	2	I54192	aminomethyltransfe
37	70	9.0	193	2	A40738	surface antigen CD
38	70	9.0	4077	2	T17484	hypothetical prote
39	69.5	8.9	385	2	AH2269	heterocyst specifi
40	69.5	8.9	479	2	F70965	hypothetical prote
41	69	8.8	260	2	T30236	methyltransferase
42	69	8.8	601	2	T49752	hypothetical prote
43	69	8.8	1369	2	D86178	hypothetical prote
44	69	8.8	1560	2	T09202	probable tail comp
45	68.5	8.8	217	2	F86343	hypothetical prote
46	68	8.7	167	2	B71553	hypothetical prote
47	68	8.7	234	2	A40710	CD30 ligand - huma
48	68	8.7	476	2	H82177	conserved hypothet
49	68	8.7	1680	1	C5MS	complement C5 prec
50	67.5	8.7	288	2	A83443	probable transcrip
51	67.5	8.7	356	2	T30361	occlusion-derived
52	67	8.6	292	2	T33987	hypothetical prote
53	67	8.6	466	2	AC3206	two component sens
54	67	8.6	468	2	AC3595	UDP-N-acetylglucos
55	67	8.6	473	2	B70541	hypothetical prote
56	67	8.6	528	2	D90545	atp synthase alpha
57	67	8.6	882	2	AF3036	nitrate reductase
58	67	8.6	903	2	E98249	nitrate reductase
59	67	8.6	993	2	G84632	hypothetical prote
60	66.5	8.5	213	2	AF2283	hypothetical prote
61	66.5	8.5	774	1	QRECFA	iron(III) dicitrat
62	66	8.5	357	2	B83652	hypothetical prote
63	66	8.5	413	2	T04520	hypothetical prote
64	66	8.5	675	2	E75393	hypothetical prote
65	65.5	8.4	352	2	T51835	3-methyl-2-oxobuta
66	65.5	8.4	822	2	T48570	hypothetical prote
67	65	8.3	256	2	B82076	probable general s
68	65	8.3	393	1	TVBE66	protein kinase (EC
69	65	8.3	406	2	T30650	hypothetical prote
70	65	8.3	430	2	AG2256	dihydrolipoamide S
71	64.5	8.3	157	2	S65055	coat protein - Chi
72	64.5	8.3	175	2	AE3293	hypothetical prote
73	64.5	8.3	563	2	S77533	DNA mismatch repai
74	64.5	8.3	2352	2	C83229	probable non-ribos
75	64	8.2	195	2	S44788	D2007.2 protein -
76	64	8.2	230	2	A95354	probable GntR-fami
77	64	8.2	447	2	S37844	molybdopterin-conv
78	64	8.2	457	2	T24962	odr-7 protein - Ca
79	64	8.2	692	2	H69416	conserved hypothet
80	64	8.2	1083	2	H86921	probable arabinosy
81	63.5	8.1	153	2	S50431	hypothetical prote
82	63.5	8.1	157	2	S48701	coat protein, 18K
83	63.5	8.1	185	2	S21366	actin-binding prot
84	63.5	8.1	342	2	AF3357	anthranilate phosp
85	63.5	8.1	350	2	JQ1656	ethylene-forming e
86	63.5	8.1	499	2	F86645	amidase [imported]
87	63.5	8.1	511	2	T26124	hypothetical prote
88	63.5	8.1	614	2	T10862	phaseolin G-box bi
89	63.5	8.1	756	2	A43582	surface antigen ms
90	63.5	8.1	863	2	F84504	probable retroelem
91	63	8.1	229	2	B82669	conserved hypothet
92	63	8.1	239	2	B40710	CD30 ligand - mous
93	63	8.1	303	2	T00899	hypothetical prote
94	63	8.1	1179	2	H82706	hypothetical prote
95	62.5	8.0	148	2	E84055	general stress pro
96	62.5	8.0	262	2	G87555	hypothetical prote
97	62.5	8.0	312	2	AD0779	conserved hypothet
98	62.5	8.0	475	2	D83202	alginate biosynthe
99	62.5	8.0	506	2	B87102	conserved membrane
100	62.5	8.0	513	2	T05948	cytochrome P450 77

ALIGNMENTS

RESULT 1
QWHUN
tumor necrosis factor alpha precursor [validated] - human
N;Alternate names: cachectin; TNFA
C;Species: Homo sapiens (man)
C;Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C;Accession: A93585; S36153; A93351; A44189; B61478; I53311; S62610; I54522; A01646; B23
R;Nedwin, G.E.; Naylor, S.L.; Sakaguchi, A.Y.; Smith, D.; Jarrett-Nedwin, J.; Pennica, D
Nucleic Acids Res. 13, 6361-6373, 1985
A;Title: Human lymphotoxin and tumor necrosis factor genes: structure, homology and chro
A;Reference number: A93585; MUID:86016093; PMID:2995927
A;Accession: A93585
A;Molecule type: DNA
A;Residues: 1-233 <NED>
A;Cross-references: UNIPROT:P01375; UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g37
R;Iris, F.J.M.; Bougueleret, L.; Prieur, S.; Caterina, D.; Primas, G.; Perrot, V.; Jurka
Nature Genet. 3, 137-145, 1993
A;Title: Dense Alu clustering and a potential new member of the NFkappaB family within a
A;Reference number: S36152; MUID:93272029; PMID:8499947
A;Accession: S36153
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-233 <IRI>
A;Cross-references: UNIPARC:UPI000000D745; EMBL:Z15026; NID:g37211; PIDN:CAA78745.1; PID
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1992
R;Pennica, D.; Nedwin, G.E.; Hayflick, J.S.; Seeburg, P.H.; Derynck, R.; Palladino, M.A.
Nature 312, 724-729, 1984
A;Title: Human tumour necrosis factor: precursor structure, expression and homology to l
A;Reference number: A93351; MUID:85086244; PMID:6392892
A;Accession: A93351
A;Molecule type: mRNA
A;Residues: 1-233 <PEN>
A;Cross-references: UNIPARC:UPI000000D745; GB:X02910; GB:X02159; NID:g37209; PIDN:CAA266
A;Note: this protein was isolated from the monocyte-like cell line HL-60 from a promyelo
R;Wang, A.M.; Creasey, A.A.; Ladner, M.B.; Lin, L.S.; Strickler, J.; Van Arsdell, J.N.;
Science 228, 149-154, 1985
A;Title: Molecular cloning of the complementary DNA for human tumor necrosis factor.
A;Reference number: A44189; MUID:85142190; PMID:3856324
A;Accession: A44189
A;Molecule type: mRNA
A;Residues: 1-62,'S',64-233 <WAN>
A;Cross-references: UNIPARC:UPI000002FB8A; GB:M10988; NID:g339737; PIDN:AAA61198.1; PID:
R;Fukuda, S.; Ando, S.; Sanou, O.; Taniai, M.; Fujii, M.; Masaki, N.; Nakamura, K.I.; An
Lymphokine Res. 7, 175-185, 1988
A;Title: Simultaneous production of natural human tumor necrosis factor-alpha, -beta and
A;Reference number: A61478; MUID:88301617; PMID:2841543
A;Accession: B61478
A;Molecule type: protein
A;Residues: 83-102;109-119;121-128,'X',130-131;142-144,'X',146,'XXX',150-152;159-174;180
A;Cross-references: UNIPARC:UPI00001735C7; UNIPARC:UPI00001735C8; UNIPARC:UPI00001735C9;
R;Marmenout, A.; Fransen, L.; Tavernier, J.; Van Der Heyden, J.; Tizard, R.; Kawashima,
Eur. J. Biochem. 152, 515-522, 1985
A;Title: Molecular cloning and expression of human tumor necrosis factor and comparison
A;Reference number: I53311; MUID:86030296; PMID:3932069
A;Accession: I53311
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <MAR>
A;Cross-references: UNIPARC:UPI000000D745; GB:M26331; NID:g339763; PIDN:AAA36758.1; PID:
A;Experimental source: U-937 cells
R;Takakura-Yamamoto, R.; Yamamoto, S.; Fukuda, S.; Kurimoto, M.
Eur. J. Biochem. 235, 431-437, 1996
A;Title: O-Glycosylated species of natural human tumor-necrosis factor-alpha.
A;Reference number: S62610; MUID:96202967; PMID:8631363
A;Accession: S62610
A;Molecule type: protein
A;Residues: 77-99 <TAK>
A;Cross-references: UNIPARC:UPI00001735CD
R;D'Alfonso, S.; Richiardi, P.M.
Immunogenetics 39, 150-154, 1994
A;Title: A polymorphic variation in a putative regulation box of the TNFA promoter regi
A;Reference number: I54522; MUID:94102809; PMID:7903959
A;Accession: I54522
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-8 <DAL>
A;Cross-references: UNIPARC:UPI00001735CE; GB:S68530; NID:g544751
R;Stevenson, F.T.; Bursten, S.L.; Locksley, R.M.; Lovett, D.H.
J. Exp. Med. 176, 1053-1062, 1992
A;Title: Myristyl acylation of the tumor necrosis factor alpha precursor on specific ly
A;Reference number: A59163; MUID:93018820; PMID:1402651
A;Contents: annotation; identification of myristylated lysines
R;Aggarwal, B.B.; Kohr, W.J.; Hass, P.E.; Moffat, B.; Spencer, S.A.; Henzel, W.J.; Brin
J. Biol. Chem. 260, 2345-2354, 1985
A;Title: Human tumor necrosis factor. Production, purification, and characterization.
A;Reference number: A92511; MUID:85130974; PMID:3871770
A;Contents: annotation; disulfide bond
C;Comment: Secreted from mitogen-activated macrophages within 4-24 hours after inductio
out detriment to normal cells. It can also act synergistically with interferon gamma to
C;Comment: TNF-alpha and -beta (lymphotoxin) are the products of different genes closel
ut are produced by different cell types and have different induction kinetics.
C;Genetics:
A;Gene: GDB:TNF; TNFA
A;Cross-references: GDB:120441; OMIM:191160
A;Map position: 6p21.3-6p21.3
A;Introns: 62/3; 78/1; 94/1
C;Complex: homotrimer
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; homotrimer; lipoprotein; lymphokine; mac
F;1-76/Domain: propeptide #status predicted <PRO>
F;77-233/Product: tumor necrosis factor #status experimental <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status experimental
F;81/Binding site: carbohydrate (Ser) (covalent) (partial) #status experimental
F;145-177/Disulfide bonds: #status experimental

Query Match 99.2%; Score 774; DB 1; Length 233;
Best Local Similarity 96.2%; Pred. No. 1.1e-78;
Matches 151; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINRPDYLDFAESGQVYFGIIAL 233
```

RESULT 2
S22052
tumor necrosis factor alpha precursor - baboon
C;Species: Papio sp. (baboon)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S22052
R;Sanjanwala, M.; Edwards, A.
submitted to the EMBL Data Library, September 1991
A;Description: Baboon Tumor Necrosis Factor Derived from Sequences of Genomic DNA.
A;Reference number: S22052
A;Accession: S22052
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <SAN>
A;Cross-references: UNIPROT:P33620; UNIPARC:UPI00001370C4; EMBL:X62141; NID:g38159; PID
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted

F;145-177/Disulfide bonds: #status predicted

Query Match 98.3%; Score 767; DB 1; Length 233;
Best Local Similarity 95.5%; Pred. No. 6.6e-78;
Matches 150; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||||||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFKGQGCPSTHVLLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| ||||||||||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDFAESGQVYFGIIAL 233
```

RESULT 3
S11688
tumor necrosis factor alpha precursor - cat
C;Species: Felis silvestris catus (domestic cat)
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S11688
R;McGraw, R.A.; Coffee, B.W.; Otto, C.M.; Drews, R.T.; Rawlings, C.A.
Nucleic Acids Res. 18, 5563, 1990
A;Title: Gene sequence of feline tumor necrosis factor alpha.
A;Reference number: S11688; MUID:91016860; PMID:2216740
A;Accession: S11688
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-233 <MCG>
A;Cross-references: UNIPROT:P19101; UNIPARC:UPI00001370BE; EMBL:X54000; NID:g1084; PIDN:
C;Genetics:
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

Query Match 90.6%; Score 707; DB 2; Length 233;
Best Local Similarity 88.5%; Pred. No. 3.3e-71;
Matches 139; Conservative 4; Mismatches 14; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||| |||||||||:|||||| |:||||||||||||| |||| |||:|||||||
Db         77 LRSSSRTPSDKPVAHVVANPEAEGQLQRLSRRANALLANGVELTDNQLKVPSDGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||| ||| |||||| ||||||| |||||||||||| ||||||||
Db        137 QVLFTGQGCPSTHVLLTHAISRFAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||| ||| | ||||||||||||||||||
Db        197 GGVFQLEKGDRLSTEINLPAYLDFAESGQVYFGIIAL 233
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RESULT 4
JQ1344
tumor necrosis factor alpha precursor - horse
N;Alternate names: cachectin; TNF alpha
C;Species: Equus caballus (domestic horse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JQ1344
R;Su, X.; Morris, D.D.; McGraw, R.A.
Gene 107, 319-321, 1991
A;Title: Cloning and characterization of gene TNF alpha encoding equine tumor necrosis f
A;Reference number: JQ1344; MUID:92084125; PMID:1748301
A;Accession: JQ1344
A;Molecule type: DNA
A;Residues: 1-234 <SUX>
A;Cross-references: UNIPROT:P29553; UNIPARC:UPI00001370BF; GB:M64087; NID:g164244; PIDN
C;Comment: This protein is an important proximal mediator of endotoxemia.
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 79/1; 95/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

Query Match 88.7%; Score 692; DB 1; Length 234;
Best Local Similarity 85.4%; Pred. No. 1.6e-69;
Matches 134; Conservative 10; Mismatches 13; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :|||||||||| ||||||||||||||||||: ||||||||||:| |||||||:|||||||
Db         78 LRSSSRTPSDKPVAHVVANPQAEGQLQWLSGRANALLANGVKLTDNQLVVPLDGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||||||||||||:|||| : ||||||| ||| |:|| ||| ||||||||
Db        138 QVLFKGQGCPSTHVLLTHTISRLAVSYPSKVNLLSAIKSPCHTESPEQAEAKPWYEPIYL 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||:||||||:|:||||||||||||||||
Db        198 GGVFQLEKGDQLSAEINQPNYLDFAESGQVYFGIIAL 234
```

RESULT 5
S12606
tumor necrosis factor alpha precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S12606; S17290; S18965; I46659
R;Drews, R.T.; Coffee, B.W.; Prestwood, A.K.; McGraw, R.A.
Nucleic Acids Res. 18, 5564, 1990
A;Title: Gene sequence of porcine tumor necrosis factor alpha.
A;Reference number: S12606; MUID:91016861; PMID:2216741
A;Accession: S12606
A;Molecule type: DNA
A;Residues: 1-232 <DRE>
A;Cross-references: UNIPROT:P23563; UNIPARC:UPI00001370C6; EMBL:X54001; NID:g2135; PIDN
R;Kuhnert, P.; Wuethrich, C.; Peterhans, E.; Pauli, U.
Gene 102, 171-178, 1991
A;Title: The porcine tumor necrosis factor-encoding genes: sequence and comparative ana
A;Reference number: S17289; MUID:91340150; PMID:1874444
A;Accession: S17290
A;Molecule type: DNA
A;Residues: 1-232 <KUH>
A;Cross-references: UNIPARC:UPI00001370C6; EMBL:X54859; NID:g2132; PIDN:CAA38639.1; PID
A;Note: the authors translated the codon GAG for residue 202 as Gly
R;Choi, C.S.; Molitor, T.W.; Lin, G.F.; Murtaugh, M.P.
submitted to the EMBL Data Library, January 1991
A;Description: Complete nucleotide sequence of a cDNA encoding porcine tumor necrosis f
A;Reference number: S18965
A;Accession: S18965
A;Molecule type: mRNA
A;Residues: 1-232 <CHO>
A;Cross-references: UNIPARC:UPI00001370C6; EMBL:X57321; NID:g2137; PIDN:CAA40591.1; PID
R;Pauli, U.; Beutler, B.; Peterhans, E.
Gene 81, 185-191, 1989
A;Title: Porcine tumor necrosis factor alpha: Cloning with the polymerase chain reactio
A;Reference number: I46659; MUID:90034181; PMID:2478420
A;Accession: I46659
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 44-232 <PAU>
A;Cross-references: UNIPARC:UPI000016C6F7; GB:M29079; NID:g164694; PIDN:AAA31128.1; PID
C;Genetics:
A;Introns: 62/3; 78/1; 93/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; myr

```
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-232/Product: tumor necrosis factor alpha #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;144-176/Disulfide bonds: #status predicted

  Query Match             86.3%;  Score 673.5;  DB 1;  Length 232;
  Best Local Similarity   85.4%;  Pred. No. 1.8e-67;
  Matches  134;  Conservative    9;  Mismatches   13;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:| || |||||||| :||||||| :  |||||||||:|:|||||||::|||||||
Db         77 LRSSSQT-SDKPVAHVVANVKAEGQLQWQSGYANALLANGVKLKDNQLVVPTDGLYLIYS 135

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||||:| |||||||||||||| ||||||| |||||||||||| ||||||||
Db        136 QVLFRGQGCPSTNVFLTHTISRIAVSYQTKVNLLSAIKSPCQRETPEGAEAKPWYEPIYL 195

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              |||||||  |||||||| ||||||||||||||||||
Db        196 GGVFQLEKDDRLSAEINLPDYLDFAESGQVYFGIIAL 232


RESULT 6
QWMSN
tumor necrosis factor alpha precursor - mouse
N;Alternate names: cachectin; TNF alpha
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 09-Jul-2004
C;Accession: A22908; S03791; A27303; A25164; A23127; A34251; I59058; A36696
R;Shirai, T.; Shimizu, N.; Shiojiri, S.; Horiguchi, S.; Ito, H.
DNA 7, 193-201, 1988
A;Title: Cloning and expression in Escherichia coli of the gene for mouse tumor necrosis
A;Reference number: A22908; MUID:88224564; PMID:2836146
A;Accession: A22908
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
A;Cross-references: UNIPROT:P06804; UNIPARC:UPI0000022334; GB:M20155
R;Shakhov, A.N.; Nedospasov, S.A.
Bioorg. Khim. 13, 701-705, 1987
A;Title: Molecular cloning of the genes coding for tumor necrosis factors: complete nucl
A;Reference number: S03791; MUID:87298639; PMID:3040015
A;Accession: S03791
A;Molecule type: DNA
A;Residues: 1-235 <SHA>
A;Cross-references: UNIPARC:UPI0000022334; GB:M38296; NID:g202086; PIDN:AAA40459.1; PID:
A;Note: article in Russian with English abstract
R;Semon, D.; Kawashima, E.; Jongeneel, C.V.; Shakhov, A.N.; Nedospasov, S.A.
Nucleic Acids Res. 15, 9083-9084, 1987
A;Title: Nucleotide sequence of the murine TNF locus, including the TNF-alpha-(tumor nec
A;Reference number: A93679; MUID:88067722; PMID:3684584
A;Accession: A27303
A;Molecule type: DNA
A;Residues: 1-235 <SEM>
A;Cross-references: UNIPARC:UPI0000022334; GB:Y00467; NID:g54830; PIDN:CAA68530.1; PID:g
R;Pennica, D.; Hayflick, J.S.; Bringman, T.S.; Palladino, M.A.; Goeddel, D.V.
Proc. Natl. Acad. Sci. U.S.A. 82, 6060-6064, 1985
A;Title: Cloning and expression in Escherichia coli of the cDNA for murine tumor necrosi
A;Reference number: A25164; MUID:85298296; PMID:3898078
A;Accession: A25164
A;Molecule type: mRNA
A;Residues: 1-235 <PEN>
A;Cross-references: UNIPARC:UPI0000022334; GB:M11731; NID:g202084; PIDN:AAA40458.1; PID:
R;Fransen, L.; Muller, R.; Marmenout, A.; Tavernier, J.; van der Heyden, J.; Kawashima,
Nucleic Acids Res. 13, 4417-4429, 1985
A;Title: Molecular cloning of mouse tumour necrosis factor cDNA and its eukaryotic expre
A;Reference number: A23127; MUID:85242112; PMID:2989794
A;Accession: A23127
A;Molecule type: mRNA
A;Residues: 1-235 <FRA>
A;Cross-references: UNIPARC:UPI0000022334; GB:X02611; NID:g54844; PIDN:CAA26457.1; PID:g
R;Cseh, K.; Beutler, B.
J. Biol. Chem. 264, 16256-16260, 1989
A;Title: Alternative cleavage of the cachectin/tumor necrosis factor propeptide results
A;Reference number: A34251; MUID:89380231; PMID:2777790
A;Accession: A34251
A;Molecule type: protein
A;Residues: 70-87 <CSE>
A;Cross-references: UNIPARC:UPI00001735CF
R;Caput, D.; Beutler, B.; Hartog, K.; Thayer, R.; Brown-Shimer, S.L.; Cerami, A.
Proc. Natl. Acad. Sci. U.S.A. 83, 1670-1674, 1986
A;Title: Identification of a common nucleotide sequence in the 3'-untranslated region o
A;Reference number: I59058; MUID:86149365; PMID:2419912
A;Accession: I59058
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-230,'R',232-235 <RES>
A;Cross-references: UNIPARC:UPI000016D086; GB:M13049; NID:g202082; PIDN:AAA40457.1; PID
R;Sherry, B.; Jue, D.M.; Zentella, A.; Cerami, A.
Biochem. Biophys. Res. Commun. 173, 1072-1078, 1990
A;Title: Characterization of high molecular weight glycosylated forms of murine tumor n
A;Reference number: A36696; MUID:91097531; PMID:2268312
A;Accession: A36696
A;Molecule type: protein
A;Residues: 80-85,'X',87-99 <SHE>
A;Cross-references: UNIPARC:UPI00001735D0
C;Genetics:
A;Introns: 62/3; 81/1; 97/1
A;Note: the first intron occurs in the 5'-untranslated region
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; mem
F;80-235/Product: tumor necrosis factor #status experimental <MAT>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

  Query Match             80.7%;  Score 629.5;  DB 1;  Length 235;
  Best Local Similarity   75.2%;  Pred. No. 1.5e-62;
  Matches  118;  Conservative   20;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| | | ||:||::|||||||||::|:|||||||::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||  :|||||:|| |:|||  ||||||: ||| ::|||||  ||||||||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVNLLSAVKSPCPKDTPEGAELKPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||:||||:| | ||||||||||||:|||
Db        199 GGVFQLEKGDQLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 7
A25451
tumor necrosis factor alpha precursor - rabbit
N;Alternate names: cachectin; TNF alpha
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: A25454; A25451; JS0727
R;Ito, H.; Yamamoto, S.; Kuroda, S.; Sakamoto, H.; Kajihara, J.; Kiyota, T.; Hayashi, H
DNA 5, 149-156, 1986
A;Title: Molecular cloning and expression in Escherichia coli of the cDNA coding for ra
A;Reference number: A25454; MUID:86219711; PMID:3519137
A;Accession: A25454
A;Molecule type: mRNA
A;Residues: 1-234 <ITO>
A;Cross-references: UNIPROT:P04924; UNIPARC:UPI000016C5C2; GB:M12845; NID:g165759; PIDN
R;Ito, H.; Shirai, T.; Yamamoto, S.; Akira, M.; Kawahara, S.; Todd, C.W.; Wallace, R.B.
DNA 5, 157-165, 1986
A;Title: Molecular cloning of the gene encoding rabbit tumor necrosis factor.
A;Reference number: A25451; MUID:86219712; PMID:3519138
A;Accession: A25451
A;Molecule type: DNA
A;Residues: 1-234 <IT2>
```

A;Cross-references: UNIPARC:UPI000016C5C2
A;Note: this sequence differs from that shown in having a Gln inserted between residues
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: JS0727
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-62,'Q',63-234 <SHA>
A;Cross-references: UNIPARC:UPI00001370C7; GB:M60340; GB:M35326; NID:g165754; PIDN:AAA31
C;Genetics:
A;Introns: 62/3; 80/1; 96/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;1-81/Domain: propeptide #status predicted <PRO>
F;82-234/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;83/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;147-178/Disulfide bonds: #status predicted

Query Match 80.4%; Score 627.5; DB 1; Length 234;
Best Local Similarity 77.7%; Pred. No. 2.5e-62;
Matches 122; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

```
Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||:||  || |:||||||| |||||||::|||||||::| |||||||::|||||||
Db         79 LRSASRALSDKPLAHVVANPQVEGQLQWLSQRANALLANGMKLTDNQLVVPADGLYLIYS 138

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||| | :||||||:|| ||||   ||||||| ||| ||||| ||   |||||||
Db        139 QVLFSGQGCRS-YVLLTHTVSRFAVSYPNKVNLLSAIKSPCHRETPEEAEPMAWYEPIYL 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||| |:|:|:||| ||||||||||||
Db        198 GGVFQLEKGDRLSTEVNQPEYLDLAESGQVYFGIIAL 234
```

RESULT 8
S52715
tumor necrosis factor alpha precursor - bovine (fragment)
C;Species: Bos primigenius taurus (cattle)
C;Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C;Accession: S52715
R;Mertens, B.; Gaidulis, L.
submitted to the EMBL Data Library, March 1995
A;Description: Cloning and sequence analysis of cDNAs encoding bovine CD40 ligand and bo
A;Reference number: S52715
A;Accession: S52715
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-185 <MER>
A;Cross-references: UNIPARC:UPI000016C282; EMBL:Z48808; NID:g755701; PIDN:CAA88743.1; PI
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein
F;33/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;97-129/Disulfide bonds: #status predicted

Query Match 80.4%; Score 627; DB 2; Length 185;
Best Local Similarity 77.7%; Pred. No. 2.1e-62;
Matches 122; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

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Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |: |||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         29 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 88

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| ||||||| : |||||||||||||| ||:|||| ||| ||||| ||| |||||||
Db         89 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 148

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |||||:||||||||||||
Db        149 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 185
```

RESULT 9
S24642
tumor necrosis factor alpha precursor - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I46047; S24642
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and t
A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46047
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-233 <CL2>
A;Cross-references: UNIPROT:Q06599; UNIPARC:UPI00001370B8; EMBL:Z14137; NID:g796; PIDN
C;Genetics:
A;Gene: TNFA
A;Introns: 62/3; 78/1; 94/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation; transmembrane protein
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;81/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;145-177/Disulfide bonds: #status predicted

Query Match 80.4%; Score 627; DB 1; Length 233;
Best Local Similarity 77.7%; Pred. No. 2.9e-62;
Matches 122; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

```
Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |: |||||||:  : |||:| :  ||||:||||:| |||||||::|||||||
Db         77 LRSSSQASSNKPVAHVVADINSPGQLRWWDSYANALMANGVKLEDNQLVVPADGLYLIYS 136

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| ||||||| : |||||||||||||| ||:|||| ||| ||||| ||| |||||||
Db        137 QVLFRGQGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPEWAEAKPWYEPIYQ 196

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| ||||||||| |||||:||||||||||||
Db        197 GGVFQLEKGDRLSAEINLPDYLDYAESGQVYFGIIAL 233
```

RESULT 10
JH0529
tumor necrosis factor alpha precursor - sheep
N;Alternate names: cachectin; TNF alpha
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0529; S48118; S13114; S20661
R;Green, I.R.; Sargan, D.R.
Gene 109, 203-210, 1991
A;Title: Sequence of the cDNA encoding ovine tumor necrosis factor-alpha: problems with
A;Reference number: JH0529; MUID:92112044; PMID:1765267
A;Accession: JH0529
A;Molecule type: mRNA
A;Residues: 1-234 <GRE>
A;Cross-references: UNIPROT:P23383; UNIPARC:UPI000002CD39; EMBL:X55152; NID:g1405; PIDN
A;Experimental source: alveolar macrophage
R;Nash, A.D.; Barcham, G.J.; Brandon, M.R.; Andrews, A.E.
Immunol. Cell Biol. 69, 273-283, 1991
A;Title: Molecular cloning, expression and characterization of ovine TNF-alpha.
A;Reference number: S48118; MUID:92155784; PMID:1786996
A;Accession: S48118
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-234 <NAS>
A;Cross-references: UNIPARC:UPI000002CD39; EMBL:X56756; NID:g297806; PIDN:CAA40076.1; P
R;Young, A.J.; Hay, J.B.; Chan, J.Y.C.
Nucleic Acids Res. 18, 6723, 1990
A;Title: Primary structure of ovine tumor necrosis factor alpha cDNA.
A;Reference number: S13114; MUID:91067496; PMID:2251151
A;Accession: S13114

```
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-62,64-234 <YOU>
A;Cross-references: UNIPARC:UPI000016C4EC; EMBL:X55966; NID:g1403; PIDN:CAA39437.1; PID:
A;Note: comparison with the introns of homologous sequences suggest that this is probabl
C;Superfamily: tumor necrosis factor
C;Keywords: alternative splicing; cytokine; cytotoxin; glycoprotein; lipoprotein; lympho
F;1-77/Domain: propeptide #status predicted <PRO>
F;78-234/Product: tumor necrosis factor alpha #status predicted <TUM>
F;20/Binding site: myristate (Lys) (covalent) #status predicted
F;82/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;96/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;146-178/Disulfide bonds: #status predicted

  Query Match             80.1%;  Score 625;  DB 1;  Length 234;
  Best Local Similarity   77.7%;  Pred. No. 4.8e-62;
  Matches  122;  Conservative   14;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  :: |||||||| | |||:| :  ||||:||||||:|||||||::|||||||
Db         78 LRSSSQASNNKPVAHVVANISAPGQLRWGDSYANALMANGVELKDNQLVVPTDGLYLIYS 137

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| | ||||| : |||||||||||||| ||:|||| ||| ||| ||||| |||||||
Db        138 QVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETLEGAEAKPWYEPIYQ 197

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||| |:|||:||||||||||||
Db        198 GGVFQLEKGDRLSAEINLPEYLDYAESGQVYFGIIAL 234


RESULT 11
I54490
tumor necrosis factor alpha precursor - white-footed mouse
C;Species: Peromyscus leucopus (white-footed mouse)
C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
C;Accession: I54490
R;Crew, M.D.; Filipowsky, M.E.
Immunogenetics 35, 351-353, 1992
A;Title: Sequence of the tumor necrosis factor/cachectin (TNF) gene from Peromyscus leuc
A;Reference number: I54490; MUID:92218012; PMID:1348497
A;Accession: I54490
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-235 <RES>
A;Cross-references: UNIPROT:P36939; UNIPARC:UPI00001370C5; GB:M59233; NID:g202506; PIDN:
C;Genetics:
A;Gene: PlTNF
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: glycoprotein; lipoprotein; myristylation
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted

  Query Match             79.9%;  Score 623.5;  DB 2;  Length 235;
  Best Local Similarity   75.2%;  Pred. No. 7.1e-62;
  Matches  118;  Conservative   20;  Mismatches   18;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| | : ||:||:| ||||||||::|:|||||:|::||||:||
Db         80 LRSSSQNSSDKPVAHVVANHQVDEQLEWLSRGANALLANGMDLKDNQLVIPADGLYLVYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||| |::|||||:|| ||||:  ||||||| ||| :|||||:|  ||||||||
Db        140 QVLFKGQGC-SSYVLLTHTVSRFAVSYEDKVNLLSAIKSPCPKETPEGSELKPWYEPIYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||:| | ||||||||||||||:|||
Db        199 GGVFQLEKGDRLSAEVNLPKYLDFAESGQVYFGVIAL 235


RESULT 12
S06192
tumor necrosis factor alpha precursor - goat (fragment)
N;Alternate names: cachectin; TNF alpha
C;Species: Capra aegagrus hircus (domestic goat)
C;Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
C;Accession: S06192; S41867
R;Goldstein, I.M.; Henner, D.; Talhouk, A.
submitted to the EMBL Data Library, March 1989
A;Reference number: S06192
A;Accession: S06192
A;Molecule type: mRNA
A;Residues: 1-193 <GOL>
A;Cross-references: UNIPROT:P13296; UNIPARC:UPI000016C3FD; EMBL:X14828; NID:g992; PIDN:
R;Rimstad, E.
submitted to the EMBL Data Library, January 1994
A;Reference number: S41867
A;Accession: S41867
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 36-38,'S',40-78,'A',80-88,'N',90-114,'Q',116-123,'D',125-144,'G',145-173,'I
A;Cross-references: UNIPARC:UPI000016C3FE; EMBL:X77317; NID:g452607; PIDN:CAA54523.1; P
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage; membrane protein
F;42/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;106-138/Disulfide bonds: #status predicted

  Query Match             79.6%;  Score 620.5;  DB 2;  Length 193;
  Best Local Similarity   78.3%;  Pred. No. 1.2e-61;
  Matches  123;  Conservative   13;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDXPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  |: ||||||||  | |||:| :  |||| ||||||:|||||||::|||||||
Db         38 LRSSSQASSNKPVAHVVANISAPGQLRWGDSYANALKANGVELKDNQLVVPTDGLYLIYS 97

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| | ||||| : |||||||||||||| ||:|||| ||| ||||| ||| |||||||
Db         98 QVLFRGHGCPSTPLFLTHTISRIAVSYQTKVNILSAIKSPCHRETPE-AEAKPWYEPIYQ 156

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| |||||||||:|:|||:||||||||||||
Db        157 GGVFQLEKGDRLSAEINQPEYLDYAESGQVYFGIIAL 193


RESULT 13
JU0029
tumor necrosis factor alpha precursor - rat
N;Alternate names: cachectin; TNF alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
C;Accession: JU0029; JN0868; S21674
R;Shirai, T.; Shimizu, N.; Horiguchi, S.; Ito, H.
Agric. Biol. Chem. 53, 1733-1736, 1989
A;Title: Cloning and expression in Escherichia coli of the gene for rat tumor necrosis
A;Reference number: JU0029
A;Accession: JU0029
A;Molecule type: DNA
A;Residues: 1-235 <SHI>
A;Cross-references: UNIPROT:P16599; UNIPARC:UPI000004368F
R;Kwon, J.; Chung, I.Y.; Benveniste, E.N.
Gene 132, 227-236, 1993
A;Title: Cloning and sequence analysis of the rat tumor necrosis factor-encoding genes.
A;Reference number: JN0868; MUID:94040766; PMID:8224868
A;Accession: JN0868
A;Molecule type: DNA
A;Residues: 1-235 <KWO>
A;Cross-references: UNIPARC:UPI000004368F; GB:L00981; NID:g205253; PIDN:AAA16275.1; PID
R;Estler, H.C.; Grewe, M.; Gaussling, R.; Pavlovic, M.; Decker, K.
Biol. Chem. Hoppe-Seyler 373, 271-281, 1992
A;Title: Rat tumor necrosis factor-alpha. Transcription in rat Kupffer cells and in vit
A;Reference number: S21674; MUID:92329007; PMID:1627266
A;Accession: S21674
A;Molecule type: mRNA
A;Residues: 1-38,'P',40-162,'T',164-201,'S',203-235 <EST>
A;Cross-references: UNIPARC:UPI000017086D; GB:X66539; GB:S40199; NID:g395369; PIDN:CAA47
```

```
C;Comment: Tumor necrosis factor is secreted by macrophages in response to endotoxin and
C;Genetics:
A;Gene: TNF-alpha
A;Introns: 62/3; 81/1; 97/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lipoprotein; lymphokine; macrophage; memb
F;80-235/Product: tumor necrosis factor #status predicted <MAT>
F;19,20/Binding site: myristate (Lys) (covalent) #status predicted
F;84/Binding site: carbohydrate (Ser) (covalent) #status predicted
F;86/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;148-179/Disulfide bonds: #status predicted

  Query Match             78.8%;  Score 614.5;  DB 2;  Length 235;
  Best Local Similarity   74.5%;  Pred. No. 7.2e-61;
  Matches  117;  Conservative   19;  Mismatches   20;  Indels    1;  Gaps    1;

Qy          1 VRSSSRTPSDKPVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYS 60
              :||||:  || |||||||| ||| ||:||::|||||||||::|:|||||||::|||||||
Db         80 LRSSSQNSSDKPVAHVVANHQAEEQLEWLSQRANALLANGMDLKDNQLVVPADGLYLIYS 139

Qy         61 QVLFXGQGCPSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYL 120
              |||| |||||  :||||||:|| |:|||  |:||||| ||| ::|||||  |||||:||
Db        140 QVLFKGQGCPD-YVLLTHTVSRFAISYQEKVSLLSAIKSPCPKDTPEGAELKPWYEPMYL 198

Qy        121 GGVFQLEXGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
              ||||||| || ||||:| | |||  |||||||||:|||
Db        199 GGVFQLEKGDLLSAEVNLPKYLDITESGQVYFGVIAL 235


RESULT 14
JH0309
tumor necrosis factor beta precursor - rabbit
N;Alternate names: lymphotoxin; TNF beta
C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: JH0309; PN0098
R;Shakhov, A.N.; Kuprash, D.V.; Azizov, M.M.; Jongeneel, C.V.; Nedospasov, S.A.
Gene 95, 215-221, 1990
A;Title: Structural analysis of the rabbit TNF locus, containing the genes encoding TNF-
A;Reference number: JH0309; MUID:91065534; PMID:2249779
A;Accession: JH0309
A;Molecule type: DNA
A;Residues: 1-197 <SH2>
A;Cross-references: UNIPROT:P10154; UNIPARC:UPI00001370CE; GB:M60340; GB:M35326; NID:g16
R;Shakhov, A.N.; Kuprash, D.V.; Turetskaya, R.L.; Azizov, M.M.; Andreyeva, A.V.; Nedospa
Mol. Biol. (Mosk.) 23, 1743-1750, 1989
A;Title: Cloning and structural analysis of the genes, coding for rabbit tumor necrosis
A;Reference number: PN0098; MUID:90220566; PMID:2633043
A;Accession: PN0098
A;Molecule type: mRNA
A;Residues: 1-197 <SHA>
A;Cross-references: UNIPARC:UPI00001370CE; GB:X55745; NID:g297167; PIDN:CAA39275.1; PID:
C;Genetics:
A;Introns: 25/3; 61/1
C;Superfamily: tumor necrosis factor
C;Keywords: cytokine; cytotoxin; glycoprotein; lymphokine; macrophage
F;1-26/Domain: signal sequence #status predicted <SIG>
F;27-197/Product: lymphotoxin #status predicted <MAT>

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  Matches   59;  Conservative   20;  Mismatches   60;  Indels   11;  Gaps    4;

Qy         12 PVAHVVANPQAEGQLQWLNRRANALLANGVELRDNQLVVPSEGLYLIYSQVLFXGQGCP- 70
              | ||:| :| |:  |:|      | | :|  | :| |:||| ||| :||||:| |:||
Db         55 PAAHLVGDPSAQDSLRWRANTDRAFLRHGFSLSNNSLLVPSSGLYFVYSQVVFSGEGCSP 114

Qy         71 ---STHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
                 | : | | :   :  |   | ||||  | |    |:|    ||   :| | || |
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Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        169 QGDQLSTHTDGIAHLLLSPS-SVFFGAFAL 197


RESULT 15
S24641
lymphotoxin - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: I46046; S24641
R;Cludts, I.; Cleuter, Y.; Kettmann, R.; Burny, A.; Droogmans, L.
Cytokine 5, 336-341, 1993
A;Title: Cloning and characterization of the tandemly arranged bovine lymphotoxin and t
A;Reference number: I46046; MUID:94083525; PMID:8260599
A;Accession: I46046
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-204 <CL2>
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C;Genetics:
A;Introns: 32/3; 68/1
C;Superfamily: tumor necrosis factor

  Query Match             31.5%;  Score 245.5;  DB 1;  Length 204;
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Qy         70 --PSTHVLLTHTISRIAVSYQTXVNLLSAIXSPCQRETPEGAEAXPWYEPIYLGGVFQLE 127
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Qy        128 XGDRLSAEINRPDYLDFAESGQVYFGIIAL 157
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Db        176 RGDQLSTHTDGISHLLLSPS-SVFFGAFAL 204


Search completed: April  3, 2006, 08:22:29
Job time : 20 secs
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